







RESULT	7	STANDARD;	PRT;	500 AA.				
ID	CPD4_RAT							
AC	P13108; DT 01-JAN-1990 (REL. 13, CREATED) DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)							
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)							
DE	CYTOCHROME P450 IID4 (EC 1.14.14.1) (P450-CMF3) (DEBRISOQUINE 4-HYDROXYLASE).							
GN	CYP2D14 OR CYP2D-4.							
OS	RATTUS NORVEGICUS (RAT).							
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUKARYOTA; RODENTIA.							
RN	[1] SEQUENCE FROM N.A.							
RP	STRAIN=SPPAGUE-DAWLEY; TISSUE=LIVER;							
RC	MEDLINE; 90189165.							
RX	MATSUMAGA E., UMEMO M., GONZALEZ F. J. ; J. MOL. EVOL. 30:155-169(1990).							
RL	[2] RP SEQUENCE OF 177-500 FROM N.A.							
RP	90050091.							
RX	ISHIDA N., TANAKA Y., INUZUKA C., SUGITA O., KUBOTA I., NAKAZATO H., NOGUCHI T., SASSA S.; BIOCHEM. BIOPHYS. RES. COMMUN. 156: 681-688(1988).							
RA	-!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.							
CC	-!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + OXIDIZED FLAVOPROTEIN + H(2)O.							
CC	-!- INDUCTION: P450 CAN BE INDUCED TO HIGH LEVELS IN LIVER AND OTHER TISSUES BY VARIOUS FOREIGN COMPOUNDS, INCLUDING DRUGS, PESTICIDES, AND CARCINOGENS.							
CC	-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.							
EMBL	X53029; G57816; -.							
EMBL	M23331; G203830; -.							
DR	D31579; D31579.							
PIR	S16677; S16773.							
DR	PROSITE; PS00086; CYTOCHROME-P450; 1.							
KW	OXIDOREDUCTASE; MONOOXYGENASE; ELECTRON TRANSPORT; MEMBRANE; HEME; MICROsome.							
FT	BINDING 446 446 HEME (BY SIMILARITY).							
SQ	SEQUENCE 500 AA; 56697 MW; 429827 CRC32;							
Query	Match 4.8%; Score 100; DB 1; Length 500;							
Best	Local Similarity 26.7%; Pred. No. 3.99e-02; Mismatches 22; Indels 4; Gaps 3;							
Matches	16; Conservative							
Db	173 FPFS-PNTLIDKAVCNVIAISLFLAAGR-FEYNDPRETRLL--DLKDTLLEESGFPLMLN 228							
Qy	6 FFLFGQDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLIGHETMKEVLEQAGANIPLYMK 65							
RESULT	8	STANDARD;	PRT;	724 AA.				
ID	KS61_MOUSE							
AC	P18553; DT 01-NOV-1990 (REL. 16, CREATED) DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)							
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)							
DE	RIBOSOMAL PROTEIN S6 KINASE II ALPHA 1 (EC 2.7.1.-) (S6KII-ALPHA)							
DE	(P90-RSK 1).							
GN	RPSSK1 OR RSK1.							
OS	MUS MUSCULUS (MOUSE).							
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUKARYOTA; RODENTIA.							
RN	[1] SEQUENCE FROM N.A.							
RP	MEDLINE; 89384612.							
RX	ALCORTA D.A., CRENS C.M., SWEET L.J., BANKSTON L., JONES S.W., ERIKSON R.L. ;							
RA	01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)							
RESULT	10	STANDARD;	PRT;	520 AA.				
ID	ION3_CARAU							
AC	P18520; DT 01-NOV-1990 (REL. 16, CREATED) DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)							



CC STRANDED DNA IN AN ATP-DEPENDANT MANNER AND ALSO CATALYZES THE  
 CC INVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED  
 CC DNA RINGS, INCLUDING CATEPANES AND KNOTTED RINGS.  
 CC -!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING  
 CC OF DOUBLE-STRANDED DNA.  
 CC -!- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA  
 CC BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE  
 CC ENZYME FORMS AN A2B2 TETRAMER.  
 DR EMBL: D73436; G1322131; ".  
 DR EMBL: D73421; G1322101; ".  
 DR PROSITE; PS00177; TOPOISOMERASE\_II; 1;  
 KW TOPOISOMERASE; ISOMERASE; ATP-BINDING; ANTIBIOTIC RESISTANCE.  
 FT NON\_TER 1  
 FT NON\_TER 116 216 216 AA; 23775 MW; E572EE00 CRC32;  
 SQ SEQUENCE 216 AA; 23775 MW; E572EE00 CRC32;

Query Match 14 Score 4.3%; Score 90; DB 1; Length 216;  
 Best Local Similarity 26.3%; Pred. No. 1.29e+00;  
 Matches 20; Conservative 23; Mismatches 26; Indels 7; Gaps 7;

DB 79 LARRIRESFLNAGVRILRDERVALEHIFDLEVGLESEKSAALDIAGLPGKKA-DCQEKD 136  
 DE 176 LALKVKETTYINRDTKILL-ETK-S-KTIVKLN-GVSEDRLLKKSVLWKLDSLOCCTERN 231  
 Db 137 PAUSELVIVEGDSAGG 152  
 Qy 232 -DINAPYLVMGGQKGG 246

RESULT 14 STANDARD PRT; 262 AA.  
 ID VIRF\_SHIDY STANDARD PRT; 262 AA.  
 AC 004248;  
 DT 01-JUN-1994 (REL. 29, CREATED)  
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE VIRULENCE REGULON TRANSCRIPTIONAL ACTIVATOR VIRF.  
 GN SHIGELLA DYSENTERIAE, SHIGELLA FLEXNERI, AND SHIGELLA SONNELL.  
 OS PLASMID 210 KB INVASION.  
 OC PROKAROTIA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 OC ENTEROBACTERIAE.  
 RN [1] SEQUENCE FROM N. A.  
 RC SPECIES=S.DYSENTERIAE; STRAIN=CG097;  
 RA YAO R., REDDY L.V., PALCHAUDHURI S.;  
 RL SUBMITTED (MAR-1991) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [2] SEQUENCE FROM N. A.  
 RP SEQUENCE FROM N. A.  
 RX MEDLINE: 87032409;  
 RA SAKAI T., SASAKAWA C., MAKINO S., YOSHIKAWA M.;  
 RL INFECT. IMMUN. 54:395-402 (1986).  
 RN [3] SEQUENCE FROM N. A.  
 RP SIMILARITY TO ARAC FAMILY.  
 RX MEDLINE: 9226642.  
 RA DORMAN C.J.;  
 RL NOL. MICROBIOL. 6:1575-1575 (1992).  
 CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF THE VIRB GENE WHICH IS  
 CC ITSELF AN ACTIVATOR OF THE IAA8BCD VIRULENCE REGULON.  
 CC -!- SIMILARITY: BELONGS TO THE ARAC/XYL5 FAMILY OF TRANSCRIPTIONAL  
 CC REGULATORS.  
 EMBL: X58464; G46954;  
 DR EMBL: M29172; G152801; -.  
 DR EMBL: X16661; G47067; -.  
 DR PIR: S14646; S14646.  
 DR PIR: A47605; A47605.

DR PIR; A60105; A60105.  
 DR PROSITE; PS00041; HTH\_ARAC\_FAMILY\_1; 1.  
 DR PROSITE; PS01124; HTH\_ARAC\_FAMILY\_2; 1.  
 KW PLASMID; VIRULENCE; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING.  
 FT H-T-H MOTIF (BY SIMILARITY).  
 DNA\_BIND 177 196  
 SQ SEQUENCE 262 AA; 11339B38 CRC32;

Query Match 4.3%; Score 89; DB 1; Length 262;  
 Best Local Similarity 25.5%; Pred. No. 1.79e+00;  
 Matches 13; Conservative 21; Mismatches 15; Indels 2; Gaps 2;

Db 37 TLTDDEGGQIAFERNQINQVNSVIKSDSINPEEFLSLDRNLLSLIRMEPI 87  
 Qy 175 ALKIRVKETTYINRDTKILLETK-SKTYKLNGVS-ERDLKKSVLWKLDSL 223

RESULT 15 STANDARD PRT; 263 AA.  
 ID KSGA\_MYCPN STANDARD PRT; 263 AA.  
 AC P75113;  
 DT 01-NOV-1997 (REL. 35, CREATED)  
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE DIMETHYLADEOSYL (RNA) TRANSFERASE (EC 2.1.1.-) (S-ADENOSYLMETHIONINE-6'-N',  
 DE N'-ADENOSYLN (RNA) DIMETHYLTRANSFERASE) (16S RNA DIMETHYLASE) (HIGH  
 DE LEVEL KASUGAMICIN RESISTANCE PROTEIN KSGA) (KASUGAMICIN  
 DE DIMETHYLTRANSFERASE).  
 GN KSGA.  
 OS MYCOPLASMA PNEUMONIAE.  
 OC PROKARYOTA; Tenericutes; MOLICUTES; MYCOPLASMA; MYCOPLASMATALES;  
 OC MYCOPLASMATACEAE.  
 RN [1] SEQUENCE FROM N. A.  
 RP STRAIN=ATCC 29142 / M129;  
 RC MEDLINE; 97103885.  
 RX HUMMELREICH R., HILBERT H., PLAGENS H., PIRKL E., LI B.-C.,  
 RA HERMANN R.;  
 RL NUCLEIC ACIDS RES. 24:4420-4429 (1996).  
 CC -!- FUNCTION: SPECIFICALLY DIMETHYLATES TWO ADJACENT ADENOSINES IN THE 3'OS  
 CC LOOP OF A CONSERVED HAIRPIN NEAR THE 3'-END OF 16S RNA IN THE 30S  
 CC PARTICLE. ITS INACTIVATION LEADS TO KASUGAMICIN RESISTANCE  
 CC (BY SIMILARITY).  
 CC -!- SIMILARITY: STRONG TO OTHER BACTERIAL KSGA.  
 CC -!- SIMILARITY: BELONGS TO THE RNA ADENINE N-6-METHYLTRANSFERASE  
 CC FAMILY.  
 DR EMBL: AE000017; G1673824; -.  
 DR PROSITE; PS01131; RNA\_A-DIMETH; 1.  
 KW RNA PROCESSING; TRANSFERASE; METHYLTRANSFERASE;  
 KW ANTIBIOTIC RESISTANCE.  
 SQ SEQUENCE 263 AA; 29794 MW; 357AA00D CRC32;

Query Match 4.3%; Score 90; DB 1; Length 263;  
 Best Local Similarity 37.0%; Pred. No. 1.29e+00;  
 Matches 20; Conservative 11; Mismatches 20; Indels 3; Gaps 3;

Db 52 KLOLPYHGTEL-DKRLAEVLLVNEBILTBQLTGDAKQNLDYFPDPIPLCG 104  
 Qy 26 NLQL-CHGEYQNMRLPN-LIGHTETMKVLEQAGAWIPLVWMOCHPTDKFQLC 77

Search completed: Thu Oct 22 15:57:09 1998  
 Job time : 47 secs.

A vertical column of five Chinese characters, each consisting of a dashed-line outline with a solid-line stroke inside. The characters are arranged vertically from top to bottom. The first character is 'Wu' (舞), the second is 'Shu' (舞), the third is 'Shi' (舞), the fourth is 'Wu' (舞), and the fifth is 'Shi' (舞). To the right of the column, the characters 'WU' and 'SHI' are written in a solid line, indicating the correct stroke order for writing the characters.

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proteins - protein database search, using Smith-Waterman algorithm

Run on:	Thu Oct 22 15:54:43 1998;	MasPar time 9.36 Seconds
Database output not generated.		509.723 Million cell updates/sec

Title: >US-08-848-439-2  
 Description: (21-295) from US08848439-pep  
 Invention: 234  
 Sequence: 1 MLQGEGSLLFLFLASHCCLGQ.....WQKGOREFKRISRSRKLQC 295

scoring table: PAM 150

Gap 11

searched: 131922 seqs, 16180660 residues  
post-processing: Minimum Match 0%  
Starting first 45 summaries

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database: a-geenesq32
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29
30:part30

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, mean 33.44, variance 132.00, scale 0.222

Result No.	Query				Database				Description		Pred. No.
	Score	Match	Length	ID	DB	Length	ID	DB	Prot	Prot	
1	396	17.7	572	27	W31273				Mouse frizzled-7	prot	2.72e-28
2	394	17.6	685	27	W1214				Mouse frizzled-8	prot	4.35e-28
3	374	16.7	585	27	W31217				Human frizzled-5	prot	4.69e-26
4	369	16.5	537	27	W31220				Mouse frizzled-4	prot	1.51e-25
5	357	15.9	525	27	W31269				Cenorhabditis frizzl	2	4.66e-24
6	355	15.9	694	27	W31287				Drosophila frizzled-2	3	9.2e-24
7	317	14.2	666	27	W31268				Mouse frizzled-3	prot	2.56e-20
8	284	12.7	709	27	W31272				Mouse frizzled-6	prot	4.86e-17
9	148	6.6	581	14	R74187				Chick p75.	3.74e-04	
10	124	5.6	605	14	R74186				Chick p78.	4.55e-02	
11	121	5.4	604	28	W35946				Human netrin-1.	8.16e-02	
12	105	4.7	529	14	R74188				Mouse p78.	1.70e+00	
13	100	4.5	732	25	W26624				Human ROCK cancer-inh	4.26e+00	
14	99	4.4	804	29	W55368						
15	96	4.3	868	25	W66610				H. pylori ORF 09ap014	5.11e+00	
16	96	4.3	868	25	W26597				Rat muscle-specific k	8.79e+00	
17	95	4.3	869	25	W26611				Rat Dm <sub>k</sub> receptor.	8.79e+00	
18	95	4.3	869	25	W26612				Human muscle-specific	1.05e+01	

				T. niveum Cyclosporin	
97	4.3	15281	9	R44929	7.34e+00
				R84094	1.26e+01
				PR18	1.50e+01
				Mouse muscle-localise	1.50e+01
				Mouse muscle-localise	1.50e+01
				Mouse muscle-localise	1.50e+01
				PR18 fusion protein.	4.28e+01
				PR18 extracellular do	3.60e+01
				Ri parameoplasmatic ant	4.28e+01
				Human TIRBP2.	4.98e+01
				Human acidic sequence o	3.60e+01
				hNET sequence encoded	3.60e+01
				Insulin-stimulated pr	3.60e+01
				Mutant insulin-stimul	3.60e+01
				NSK2 receptor with al	3.60e+01
				NSK2 receptor with al	3.60e+01
				NSK2 receptor with al	3.60e+01
				NSK2 receptor with al	3.60e+01
				Neuronal invertebrate	3.60e+01
				Invertebrate calcium	3.60e+01
				Human type I inositol	4.28e+01
				Human T cell inositol	4.28e+01
				Inositol-3-phosphate	4.28e+01
				ODC.	7.15e+01
				NK-lysine full length	8.47e+01
				Rat polylysaccharide in	1.00e+02
				Rat spleen pro-hormon	8.47e+01

## ALIGNMENTS

RESULT 1

LD W31273 Standard; Protein; 3/2 AA.  
 AC W31273;  
 DT 27-APR-1998 (first entry)  
 DE Mouse frizzled-7 protein Mfz7 (Wnt receptor).  
 KW Wnt receptor; mouse frizzled-7 protein; Mfz7 gene;  
 KW signal transduction; cancer; cell growth; cell proliferation.

PN WO9739357-A1.

PD 23-OCT-1997; U06049.

PF 11-APR-1996; US-015307.

PR 12-APR-1996; US-015307.

PA (UYJO ) UNIV JOHNS HOPKINS.

PA (STRD ) UNIV LEELAND STANFORD JUNIOR.

PI Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J,

PI Nusse R, Samos CH, Wang Y;

WPI; 97-526631/48.

DR N-PSDB; T83891.

PT Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation related disorders

PT Disclosure; Page 44-46; 61pp; English.

PS This protein comprises the mouse transmembrane receptor, frizzled 7 (Mfz7), encoded by the *Mfz7* gene (see T89891). It is an example of a Wnt receptor. Other novel frizzled family members have been identified in human, mouse and *Caenorhabditis elegans* (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.

Sequence	3'2' RA;
Query Match	Score 396; DB 27; Length 572;
Best Local Similarity	Pred. No. 2 72e-28;
Matches	Mismatches 42; Indels 3; Gaps
48; Conservative	25;
Db 51 pisiplectdalyngtqtilpnllghtqedaglevhgyplkvgqcspelrfflclsmyapvc 110	

Qy	44 PANLQLCHGTEYQNNRPLNLLIGHTMKEVLEQAGAWIPLYNRQCHPDTKFLCSLFAPVC 103
Db	111 -tvldqappcrs1ceraggeal1nnk gfgfqwpver1rcnfpvhagecivygqntsd 167
Qy	104 LDDLETTIOCHSLCYOKVYKDCAPNSAEGRPWPDMLCDEP-ODN-DLCTPLASSD 159

(STRD) UNIV LELAND STANFORD JUNIOR.  
Andrew D, Bhamot P, Brink M, Hsieh J, Nathans J,  
Nusse R, Samos CH, Wangy;  
WPI; 97-526631/48.  
N-PSDR: T89889.

RESULT	2
ID	W31274 standard; Protein: 685 AA.
AC	W31274;
DT	27-APR-1998 (first entry)
DE	Mouse frizzled 8 protein <i>Mfz8</i> (Wnt receptor).
KW	Wnt receptor; mouse frizzled-8 protein; <i>Mfz8</i> gene;
KW	signal transduction; cancer; cell growth; cell proliferation.
OS	Mus musculus.
PN	W09739357 A1.
PD	23-OCT-1997.
PF	11-APR-1997; U06049
PR	12-APR-1996; US105407.
PA	(UYJO ) UNTV JOHNS HOPKINS.
PA	(STRD ) UNTV LEELAND STANFORD JUNIOR.
PA	Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J,
PI	Nusse R, Samos CH, Wangy;
PI	WPI: 97-566631/48.
DR	N-PSDB; 189892.
PT	Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation related disorders
PT	Disclosure; Page 48-50; 61PP; English.
PS	This protein comprises the mouse transmembrane receptor, frizzled-8 ( <i>Mfz8</i> ), encoded by the <i>Mfz8</i> gene (see W89892). It is an example of a Wnt receptor. Other novel frizzled family members have been identified in human, mouse and <i>Caenorhabditis elegans</i> (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.

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Qry	Db	Accession	Best Local Similarity	Prod. No.	Length	Indels	Gaps
Qy	Db	Q96384	32%	35%	375	0	0
Qy	Db	Q96384	43.8%	4.35E-28	350	6	6
Qy	Db	Q96384	56%	Conservative	23	Mismatches	43
Qy	Db	Q96384	40	vpvlchgignyntymqnfqnhdtqdagglevhqfw-piveiqspdkfficsmytpcile	98		
Qy	Db	Q96384	47	LQJGKPLPQEIQNMRFLNLGETMKR-LEQAGAWPLVMQCHPDKKFLPFLFVCLD	105		
Qy	Db	Q96384	99	dykkpklppcrsverakagcaplmrgqfawpdmrccdr1peqqgpd1cmndyntd-1t	157		
Qy	Db	Q96384	106	DLDETIQPCSLCVOYKDRCAPVMSAFGFPWDMLECDREP-QDN-D-ICIPASSDHLL	162		
Qy	Db	Q96384	158	taapsppi	165		
Qy	Db	Q96384	163	PATEEAPK	170		

RESULT      3  
 ID      W31271 standard; Protein: 585 AA.  
 W31271;  
 AC      W31271;  
 DT      27 APR 1998 (first entry)  
 DE      Human frizzled-5 protein Nfz5 (Wnt receptor).  
 KW      Wnt receptor; human frizzled-5 protein; Nfz5 gene;  
 KW      signal transduction; cancer; cell growth; cell proliferation.

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PA	(STRD ) UNIV LEELAND STANFORD JUNIOR.
PI	Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J,
PI	Nusse R, Samos CH, Wangy;
DR	WPI: 97-526631/48.
DR	N-PSDB: T88889.
PT	Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation related disorders
PT	Disclosure: Page 37-39; 61pp; English.
PS	This protein comprises the human transmembrane receptor, frizzled-5 (Hfz5), encoded by the Hfz5 gene (see T88889). It is an example of a Wnt receptor. Other novel frizzled family members have been identified in human, mouse and <i>Caenorhabditis elegans</i> (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.
SQ	585 AA;
Query Match	16.7%; Score 374; DB 27; Length 585;
Best Local Similarity	38.8%; Pred. No. 4.69e-26;
Matches	47; Conservative 29; Mismatches 41; Indels 4; Gaps 4;
CC	This protein comprises the human transmembrane receptor, frizzled-5 (Hfz5), encoded by the Hfz5 gene (see T88889). It is an example of a Wnt receptor. Other novel frizzled family members have been identified in human, mouse and <i>Caenorhabditis elegans</i> (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.
CC	585 AA;
Db	20 lvgraaasakapvcqei-t-vpmcrqgignlynlhmpnqfnhdtgdeaglevhafw-pivei 76
Qy	27 LFQQPPFSYRSNCRPPIPANLQLQHGTIEQNMRPLPFLGHETKREV-EQAGAWIPPMVK 85
Db	77 qcspdpdrffcttmytrpicipldyhplppcrscearakgcsplmrqyfawpermssdr1 136
Qy	86 QCHPDRKTKELFLSFAPVCLLDDLETTIOPCHSLCYQVKDRCAPMSAFGPWMDLCEDRF 145
Db	137 P 137
Qy	146 P 146
RESULT	4
ID	W31270 standard: Protein: 537 AA.
AC	W31270;
DT	27-APR-1998 (first entry)
DE	Mouse frizzled-4 protein Mfz4 (Wnt receptor).
KW	Wnt receptor; mouse frizzled-4 protein; Mfz4 gene;
KW	signal transduction; cancer; cell growth; cell proliferation.
OS	Mus musculus.
PN	W09730357-21.
PD	23-OCT-1997.
PF	11-APR-1997; US06049.
PR	12-APR-1996; US-0153-07.
PA	(UYJO ) UNIV JOHNS HOPKINS.
PA	(STRD ) UNIV LEELAND STANFORD JUNIOR.
PI	Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J,
PI	Nusse R, Samos CH, Wangy;
DR	WPI: 97-526631/48.
DR	N-PSDB: T88889.
PT	Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation related disorders
PT	Disclosure: Page 34-35; 61pp; English.
PS	This protein comprises the mouse transmembrane receptor, frizzled-4 (Mfz4), encoded by the Mfz4 gene (see T88888). It is an example of a Wnt receptor. Other novel frizzled family members have been identified in human, mouse and <i>Caenorhabditis elegans</i> (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.
CC	585 AA;
CC	This protein comprises the mouse transmembrane receptor, frizzled-4 (Mfz4), encoded by the Mfz4 gene (see T88888). It is an example of a Wnt receptor. Other novel frizzled family members have been identified in human, mouse and <i>Caenorhabditis elegans</i> (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.
CC	585 AA;

CC treatment of diseases related to these conditions.  
Sequence 537 AA;

Query Match 16.5%; Score 369; DB 27; Length 537;  
Best Local Similarity 38.3%; Pred. No. 1.51e-25;  
Matches 41; Conservative 26; Mismatches 40; Indels 0; Gaps 0;  
Db 47 piriamcqgnvntkmpnlgvghlqlttaelqtlqfplqyccsqqlqfflcsvvypmc 106  
Qy 44 PANLQLQGIEQNMRPLNLLGHTMKEYLQAGAWIPLVMQCHPDTKFLCSLFAPVC 103

Db 107 tekinipigpcggmcslsvkrrecpvlrefgfaawpdtdlncskfpqnd 153

Qy 104 LDLDDETIQPCHSLCQVQRDRCAPVMSAFGEFPWPDMLECDRFQND 150

RESULT 5  
ID W31269 standard; Protein: 525 AA.

AC W31269;

DT 27-APR-1998 (first entry)

DE Caenorhabditis frizzled-1 protein Cfrz1 (Wnt receptor).  
KW Wnt receptor; Caenorhabditis frizzled-1 protein; Cfrz1 gene;

KW signal transduction; cancer; cell growth; cell proliferation.  
OS Caenorhabditis elegans.

PN W0739357-A1.

PD 23-OCT-1997;

PR 23-OCT-1997;

PR 11-APR-1996; US-015307.

PA (UYJO ) UNIV JOHNS HOPKINS.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J,

PI Nusse R, Santos CH, Wangy;

DR WPI; 97-516631/48.

DR N-PSDB; T89887.

PR Identification of Wnt receptor binding modulators - useful for

PT treatment of cancer and growth, development or proliferation related

PT disorders

PS Disclosure: Page 30-31; 61pp; English.

CC This protein comprises the Caenorhabditis putative transmembrane receptor, frizzled-1, encoded by the cfrz gene (see T89887). It is an example of a Wnt receptor. Other novel frizzled family members have been identified in human, mouse and Caenorhabditis elegans (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.

Sequence 525 AA;

Query Match 16.0%; Score 357; DB 27; Length 525;

Best Local Similarity 31.8%; Pred. No. 2.46e-24;

Matches 54; Conservative 51; Mismatches 57; Indels 8; Gaps 8;

Db 32 emendipnlnitsfpnlnvadaseslityplisvcsqkfflcsyfpmcnakl 91

Qy 48 QLICHGIEQNMRPLNLLGHTMKEYLQAGAWIPLVMQCHPDTKFLCSLFAPVCDDL 107

Db 92 anpigpcrpclsvqekcplvlesfgfkwpdvlrcdkfplnenrekcmnk-gpnegg-ai 149

Qy 108 DETQPCHSLCQVQRDRCAPVMSAFGEFPWPDMLECDRFQND 164

Db 150 qderakf-aa-keseddndrvediqrevdr1ngkcpqdevflnrsskcv 197

Qy 165 TEEAPKVEACKNKKNDNDIMETLCKNDFAKIKV-KEITYINRDTKII 213

RESULT 6  
ID W31267 standard; Protein: 694 AA.

AC W31267;

DT 27-APR-1998 (first entry)

DE Mouse frizzled-3 protein Mfz3 (Wnt receptor).

RESULT 7  
ID W31268 standard; Protein: 666 AA.

AC W31268;

DT 27-APR-1998 (first entry)

DE Mouse frizzled-3 protein Mfz3 (Wnt receptor).

DE Drosophila frizzled-2 protein (Wnt receptor). Dfz2 gene;  
KW Wnt receptor; Drosophila frizzled-2 protein; signal transduction; cancer;  
KW wingless receptor; Wg receptor; cell proliferation.

OS Drosophila melanogaster.

Key Location/Qualifiers  
Misc\_difference 268

FT Misc\_difference "note- "encoded by CAC"

FT Misc\_difference 269  
FT Misc\_difference "note- "encoded by TGG"

FT Misc\_difference 348  
FT Misc\_difference "note- "encoded by TA (apparent 1 nucleotide deletion of codon)"

FT Misc\_difference 488  
FT Misc\_difference "note- "encoded by TTA"

FT Misc\_difference 632  
FT Misc\_difference "note- "encoded by CTG"

FT Misc\_difference 633  
FT Misc\_difference "note- "encoded by GCG"

FT Misc\_difference 671  
FT Misc\_difference "note- "encoded by CG (apparent 1 nucleotide deletion of codon"

FT W0739357-A1.

PN 23-OCT-1997;

PD 23-OCT-1997;

PR 11-APR-1996; US-015307.

PA (UYJO ) UNIV JOHNS HOPKINS.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J,

PI Nusse R, Santos CH, Wangy;

DR WPI; 97-516631/48.

DR N-PSDB; T89885.

PR Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation related disorders

PS Claim 2; Page 23-25; 61pp; English.

CC This protein comprises the Drosophila frizzled-2 protein encoded by the Dfz2 gene (see T89885). It is a receptor for wingless (Wg), acting as a signal transducing molecule, and is an example of a Wnt receptor (WntR). Other novel frizzled family members have been identified in human, mouse and Caenorhabditis elegans (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.

Sequence 694 AA;

Query Match 15.9%; Score 355; DB 27; Length 694;

Best Local Similarity 36.2%; Pred. No. 3.92e-24;

Matches 47; Conservative 32; Mismatches 45; Indels 6; Gaps 6;

Db 51 yggpaip-kdpnrlceetipmargigymntsfpmemnhetqdeagleyhqfw-pivalk 108

Qy 28 FGQPFDSYKRSNCRPIANIQLCHGIEQNMRPLNLLGHTMKEYLQAGAWIPLVMQCHPDTKFLCSLFAPVCDDL 107

Db 109 cspdkfklcsmtpicledyhkplpvcrsverarsgapsimqgysfewpermacehlp 168

Qy 87 CHPTDKFLCSLFAPVCDDLDETQCHSLCQVQRDRCAPVMSAFGFPPWPDMLECDRFQ 146

Db 169 1hgqpdnlcm 178

Qy 147 -Q-D-NDLCI 153

Query	Match	Length	
Best Local Matches	317; Pred. No. 2	666;	
Similarity	33.38;		
Matches	29; Conservative		
DB	5;		
27	scepi-t-lrmcqdlpynttfmpnllnhdqgtaalam-pfhpmvnlldsrdfrpfcfa	83	
DB	39	NCKPIPANIQLCHSIEKYQNMRLPNLGH-ETMKEYLEQAGAWIPLVMQCHPDTKFLCS	97
DB	84	lyapicme-ygrvrlpckrcgraysecsklmentgvpypedmcscrfpdcdepvrlyd	142
DB	98	LFAPVCLDDLETTIQPCHSICVQYRDCAPVMSAEGFPWDMLECDRFQPDNLCLPLAS	157
DB	143	lnlvgdptegap	154
DB	158	SDHLLPATEEAP	169

RESULT 8  
 ID W311272 standard: Protein; 709 AA.  
 AC W311272;  
 DT 27-APR-1998 (first entry)  
 DE Mouse frizzled-6 protein Mfz6 (Wnt receptor).  
 KW Wnt receptor; mouse; frizzled-6 protein; Mfz6 gene;  
 KW signal transduction; cancer; cell growth; cell proliferation.  
 KW Mus musculus.  
 DS

have been identified in human, mouse and *Caenorhabditis elegans* (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.

Query	Match	12.7%	Score 284;	DB 27;	Length 709;
Best Local	Similarity	33.6%	Pred. No. 4	86e-17;	
Matches		26;	Mismatches	49;	Indels 6; Gaps 6;
41; Conservative					
Db	24	cepitvp-r-cmkmtv-nmtffphnlmghydqgiaavemghfhlanespnimflcqa	80		
Qy	40	CKPVPANQLCHGTYQQNMRL-PNLIGHETMKVELEQAGAWIPLVYMKQCHPDTKFLCSL	98		
Db	81	fiptcteqih-vvlporkciksvdkkkimdtfqirwppelecnrphcddt-vptvsh	138		
Qy	99	FAPVCLDDLDDETIQPOPHSLCQVKDRCAPMSAFEGPWPDMLECRFPQONDLCIPLASS	158		
Db	139	ph	140		
Qy	159	DH	160		

RESULT	
ID	R74187 standard; Protein; 581 AA.
AC	R74187;
DT	24-DEC-1995 (first entry)
DE	Chick P75.
KW	neuronal growth modulator; epidermal growth factor; EGF;
KW	neuronal-2; p75; neurodegenerative disease; transgenic animal;
KW	gene therapy.
OS	Galus sp.
PH	
key	Location/Qualifiers
peptide	1..15
FT	/label= Sig_peptide
FT	16..260
domain	/label= Domain-VI
FT	/note= "Domain VI is probably involved in protein-
FT	protein complex formation"
domain	261..429
FT	/label= Domain-V
FT	/note= "Domain V includes EGF-like repeats"
region	430..581
FT	/note= "C-terminal region"

FN  
WO 93/33879/A1.  
PN  
18-MAY-1995.  
PD  
08-MAY-1995.  
PF  
08-MAY-1994; U12913  
PR  
12-NOV-1993; US-152019.  
PA  
(REGC ) UNIV CALIFORNIA.  
PA  
(UYCO ) UNIV COLUMBIA NEW YORK.  
PI  
Dodd J., Jessell T., Kennedy T., Placzek M., Serafini T.;  
PI  
Tessier-Lavigne M.;  
WPI: 95-194086/25.  
DR  
N-PSDB; Q92367.  
PT  
Neural axon out-growth modulators derived from EGF-like repeats of  
neuin 1 or neuin 2 - comprise peptide(s) capable of selectively  
inhibiting spinal axon out-growth or directing axon orientation  
PT  
Claim 1: Page 48-50; 58pp; English.  
CC  
An E10 chick brain cDNA library was screened with probes based on  
neuin 1 (P78) or neuin 2 (P75) sequences to isolate chick p78  
and P75 partial cDNA clones. Full-length clones (given in  
CC  
Q92366-67, respectively) were subsequently obt. by 3 RACE. cDNA  
is expressed e.g. in COS insect cells for recombinant p78 and  
CC  
P75 prodn. used to breed transgenic animals, or for gene therapy  
CC

Query	Match	Score	DB 14:	Length
Sequence	Joi An;	148;	No	581;
Best Local Similarity	6.68;	27.08;	714.04;	

Matches	30;	Conservative	28;	Mismatches	46;	Indels	7;	Gaps	6;
Db	431	ipainptslvtste-apadedsckpaqnykinmkkyckkdyygvqnilmetvanwak							489
Qy	153	IPASSDHLLPATEEAPKVCEA-CKNRNDNDIMETLCKNDFAKKVKEITYINRTD							211
Db	490	ftinils--vykcrdervrk gdnflwihlkdslscpk1 qisckylyvng							536
Qy	212	IILETKSHTKYLNGVSTERDLKSVWLK-DSLQCICEMNDINAPPILYMG							261
RESULT	10								
ID	R74186;	standard;	Protein:	605 AA.					
AC	R74186;								
DT	24-DEC-1995	(first entry)							
DE	Chick p78.								
KW	Neural axon out-growth modulator; epidermal growth factor; EGF;								
KW	neuritin; p78; neurodegenerative disease; transgenic animal;								
KW	gene therapy.								
OS	Gallus sp.								
PFH	Key peptide	Location/Qualifiers							
FFT	peptide	1..25	/label=	sig_peptide					
FFT	misc_difference	29							
FFT			/note=	"unspecified amino acid"					
FFT	misc_difference	38							
FFT			/note=	"unspecified amino acid"					
FFT	misc_difference	50							
FFT			/note=	"unspecified amino acid"					
domain	domain	26..284	/label=	Domain-VI					
FFT			/note=	"Domain VI is probably involved in protein-protein complex formation"					
domain	domain	285..453							
FFT			/label=	Domain-V					
region	region	454..605							
FTN	FTN		/note=	"domain V includes EGF-like repeats"					
FTN	FTN		/note=	"C-terminal region"					
W90513367-A1.									
PN	18-MAY-1995.								
PPD	08-NOV-1994.								
PPF	08-NOV-1994.								
PPA	12-NOV-1993.								
PA	US-15201919.								
(REGC )	UNIV CALIFORNIA.								
(UWCO )	UNIV COLUMBIA NEW YORK.								
PA	Dodd J, Jessell T, Kennedy T, Placzek M, Serafini T;								
PI	Tessier-Lavigne M;								
PI	WPI: 95-194086/25.								
DR	DR								
DR	N-PSDB; Q92366.								
PT	Neural axon out-growth modulators derived from EGF-like repeats of								
PT	neuritin 1 or neuritin 2 - comprise peptide(s) capable of selectively								
PT	increasing spinal axon out-growth or directing axon orientation								
PS	Claim 1; Page 44-46; 58pp; English.								
CC	An E10 chick brain cDNA library was screened with probes based on								
CC	neuritin 1 (p78) or neuritin-2 (p75) sequences to isolate chick p78								
CC	and p75 parental cDNA clones. Full-length clones (given in								
CC	Q92366..67, respectively) were subsequently obt'd. by 3'Race. cDNA								
CC	is expressed e.g. in COS or insect cells for recombinant p78 and								
CC	p75 prodn., used to breed transgenic animals, or for gene therapy.								
SQ	Sequence 605 AA;								
Query	Match	5.6%	Score	124;	DB	14;	Length	605;	
Best	Local	Similarity	26.1%	Pred.	NO.	4.55e-02;			
Matches	31;	Conservative	34;	Mismatches	41;	Indels	13;	Gaps	11
Db	455	ipaapppptaassteepad-cdsyckaskgk1kinmkkyckkdyygvqnilmetvanwak							512
Qy	153	IPASSDHLLPATEEAPKVCEA-CKNRNDNDIMETLCKNDFAKKVKEITYINRTD							210
Db	513	kftnitis--vyk-9g-snrlrrgdtlwvhakdiackpkvphk-y111gsts							565
Qy									
Db	513	kftnitis--vyk-9g-snrlrrgdtlwvhakdiackpkvphk-y111gsts							266
Qy	211	KIILETKSHTKYLNGVSTERDLKSVWLK-SLQCTCEEMNDINAPPILYMGQKGG							

RESULT	11	W35446; standard; Protein; 604 AA.
ID	W35446;	
AC	W35446;	
DT	11-MAY-1998	(first entry)
DE	Human neprin-1.	
KW	Neprin-1; neuron; growth; difference; neural disease; diagnosis; therapy; Homo sapiens.	
OS	Homo sapiens.	
PN	WO9100564-A1.	
PD	30-OCT-1997.	
PR	19-APR-1996; US635137.	
PA	(EXEL-) EXELIXIS PHARM INC.	
PA	UNIV CALIFORNIA (RECC)	
PI	Kennedy T, Leonardo D, Serafini T	
PI	Tessier-Lavigne M, Zhang Y;	
WPI	97-535773/49.	
DR	N-PSDB; 197129.	
PT	Human neprin-1 protein and related modulating neuron growth and secretion of diseases associated with treatment.	
PT	Claim 1; Page 13-15; 22pp; English.	
PS	This protein comprises human neprin-1 which is involved in neural axon growth and development.	
CC	CC	
SQ	Sequence 604 AA;	
Query	Query	Match Score
Best	5.4%	Local Similarity
Matches	24.8%	Pred
29;	Conservative	30;
Db	454	ipvappttaaasvve-pedcdsyckass
Qy	153	IPPLASSDHLLPATEAPKVEA-CKNKK
Db	512	kftvnlis--vykqgttsrirrgdqs-lw
Qy	211	KIILETKSKTKYIKLNGYSERDLKKVSLR
RESULT	12	R74188 standard; Protein; 529 AA.
ID	R74188;	
AC	R74188;	
DT	24-DEC-1995	(first entry)
DE	Mouse p78.	
KW	Neuronal axon out-growth modulator.	
KW	neprin-1; p78; neurodegenerative gene therapy.	
OS	Mus sp.	
FH	Key	Location/Qualification
FT	miss_difference	296..297
FT	miss_difference	300..301
FT	miss_difference	307..308
FT	miss_difference	311
FT	miss_difference	389
FT	miss_difference	393..394
FT	miss_difference	487

PN	WO9513367-A1.	Best Local Similarity 30.5%; Pred. No. 4.26e+00; Matches 25; Conservative 25; Mismatches 36; Indels 6; Gaps 5;
PD	18-MAY-1995; U12913.	
PF	08-NOV-1994; U12913.	
PR	12-NOV-1993; US-152019.	
(REGC )	UNIV CALIFORNIA.	
(UYCO )	UNIV COLUMBIA NEW YORK.	
PA	Dodd J, Jessell T, Kennedy T, Placzek M, Serafini T;	
PI	Tessier-Lavigne M;	
DR	WPI: 95-194086/25;	
DR	N-PSDB; Q92368.	
PT	Neural axon out-growth modulators derived from EGF-like repeats of netrin 1 or netrin 2 - comprise peptide(s) capable of selectively increasing spinal axon out-growth or directing axon orientation	
PT	Claim 1; Page 51;	
CC	Chick P75 and P78 sequences (given in R74186-87, respectively) were used to identify conserved amino acid regions, which were then used to design degenerate primers for the amplification of a fragment of the mouse P78 cDNA (Q92368). This cDNA can be expressed in host cells for recombinant p78 prodn, or used to breed transgenic animals, or for gene therapy.	
SQ	Sequence 529 AA;	
Query Match	4.7%; Score 105; DB 14; Length 529;	
Best Local Similarity 23.5%; Pred. No. 1.70e+00; Matches 24; Conservative 25; Mismatches 45; Indels 8; Gaps 7;		
Db	388 sxevexxedodsyckaskgklkmnnkkycrkdyavqhhilkadkagdw-wkfvtvnis.. 444	
Qy	:    :    :    :    :    :    :    :    :    :    :    :    :	
Db	163 PATEEAPKVCEA-CKNKNDNDIMETLCKNFALKIKV-KEITYINRDTK1ILETKSKT 220	
Qy	:    :    :    :    :    :    :    :    :    :    :    :	
Db	445 vykqgtsrirrgdqs-lwirsdiackopkplkk-yll1g 484	
Qy	:    :    :    :    :    :    :    :    :    :    :	
Db	221 IYKLNSVSERDUKKSVLWLKD-SLQCTCEENDINAPYLVNG 261	
Qy	:    :    :    :    :    :    :    :    :    :    :	
RESULT	13	
ID	W26642 standard; Protein: 732 AA.	
AC	W26642;	
DT	11-FEB-1998 (first entry)	
DE	Human RECK cancer-inhibiting protein.	
KW	RECK; reversion-inducing cysteine rich protein with Kazal motif; human; cancer; gene therapy; diagnosis.	
KW	Homo sapiens.	
OS		
FT	Location/Qualifiers	
FT	396..415 /label= Kazal_domain	
PN	WO974439-A1.	
PD	10-JUL-1997.	
PF	24-DEC-1996; U20812.	
PF	27-DEC-1995; JP-340469.	
PA	(AMGE-) AMGEN INC.	
PA	(KITA-) KITAYAMA, H.	
PA	(NODA-) NODA, M.	
PA	(TAKA-) TAKAHASHI, C.	
PA	(SANY-) SANKYO CO LTD.	
PI	Kitayama, H., Noda, M., Takahashi, C;	
DR	WPI: 97-363675/33.	
DR	N-PSDB; T90508.	
PT	RECK gene and corresponding protein sequences - enables reversion of cancer cells	
PS	Claim 7; Page 42-44; 53pp; English.	
CC	This protein sequence comprises the human RECK protein (reversing-inducing cysteine rich protein with Kazal motif), which is capable of transforming malignant cancer cells with an activated ras gene into normal cells (reversion activity). Its amino acid sequence was deduced from a cDNA clone (see T90508), obtained from human fibroblast MRC-5 (ATCC CCL 17) cells. A claimed method for treatment of cancer comprises contacting the cancer cells with a RECK polypeptide. RECK may also be expressed using gene therapy methods for in vivo treatment of cancer.	
CC	Sequence 732 AA;	
Query Match	4.5%; Score 100; DB 25; Length 732;	
Query Match	4.4%; Score 99; DB 29; Length 804;	
Best Local Similarity 31.5%; Pred. No. 5.11e+00; Matches 17; Conservative 17; Mismatches 19; Indels 2; Gaps 2;		
Db	78 vidsipkegftplenaaffnitysmrgggfilhikpkvmmrlifsfardykkai 131	
Qy	:    :    :    :    :    :    :    :    :    :    :    :    :	
RESULT	15	
ID	W26610 standard; Protein: 868 AA.	
AC	W26610;	
DT	27-JAN-1998 (first entry)	
DE	Rat muscle-specific kinase (MuSK).	

Receptor tyrosine kinase; muscle specific kinase; MusK; DmK; rat;  
 Ligand; agrin; diagnosis; therapy.  
 Rattus sp.  
 Key Peptide Location/Qualifiers  
 FT 1..19  
 FT /label= Sig\_peptide  
 FT 21..492 /label= Extracellular\_domain  
 FT 493..521 /label= Transmembrane\_domain  
 FT 522..868 /label= Intracellular\_domain  
 PN WO9721811-A2.  
 PD 19-JUN-1997.  
 PF 13-DEC-1996; U20696.  
 PR 10-MAY-1996; US-644271.  
 PR 15-DEC-1995; US-008657.  
 PA (REGE-) REGENERON PHARM INC.  
 PI Bowen DC, Glass DJ, Valenzuela DM, Yancopoulos GD;  
 DR 97-332783/30.  
 N-PSDB: T90472.  
 PT Nucleotide sequences encoding human agrin and muscle specific kinase  
 PT and related receptor - used in diagnosis and treatment of disorder  
 PT with muscle atrophy  
 PS Example 1: Fig 1; 120pp; English.  
 CC This polypeptide comprise a novel rat receptor tyrosine kinase  
 CC designated muscle specific kinase (MusK) that is expressed in  
 CC normal and denervated muscle. MusK is alternatively referred to  
 CC DmK for denervated muscle kinase. The amino acid sequence was  
 CC deduced from an isolated cDNA clone (see T90472). Human MusK (see  
 CC W26611) has also been identified. Use of MusK to generate anti-  
 CC MusK antibodies and in the diagnosis of neurologic or other  
 CC disorders is disclosed. Assay systems that may be used to detect  
 CC and/or measure ligands that bind the musk gene product are provided.  
 CC A claimed method of promoting the growth, differentiation or  
 CC survival of MusK receptor-expressing cells involves administration  
 CC to the cell of agrin (see W26609). Such cells include muscle,  
 CC heart, spleen, ovary and retina cells, or cells genetically  
 CC engineered to express the MusK receptor.  
 SQ Sequence 868 AA;

Query Match 4.3%; Score 96; DB 25; Length 868;  
 Best Local Similarity 29.7%; Pred. No 8.79e+00;  
 Matches 19; Conservative 12; Mismatches 28; Indels 5; Gaps 5;  
 345 eaagellihh-anelhavspicrpaaeallcnhlfqecspvvlptpmicreyclavke 403  
 67 ETMKEYLEQAGAWIPL-VMKQ-CHPDITKKFLCS-LFAPVCLDDLDERTIQPCHSLCVQVKD 123

Db 404 lfca 407

Qy 124 R-CA 126

Search completed: Thu Oct 22 15:56:03 1998  
 Job time : 80 secs.

50

Dec 3 1985

1

MATERIALS

EDGYRTVQGTTKEGGTILFMM  
QYFHLLAAWAVPAVKTITILAMGQ  
STSFLIAEGVSLFRITIMKHDT  
FREHMRWSVSQHCKSLAIPCBA  
TTHSMRKEYTRLTNSRGETTV"

`bb_xref=pid:931013`

**bb\_xref=**pid:931013

osteosarcoma cDNA to  
zoa; Chordata; M. Bradley, M.S.,  
h; Myomorpha; Muridae;  
D., Strelcer, G.J. and  
one frizzled (fz) are

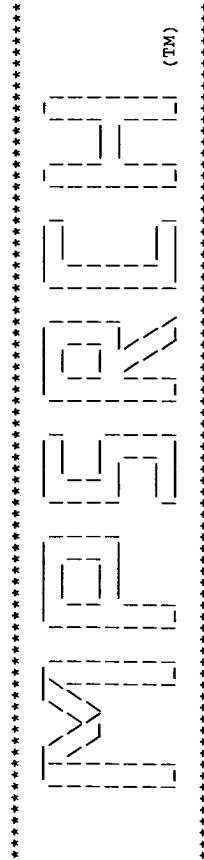
RESULT 12  
ID CER23D8 standard; DNA; INV; 34576 BP.

NI	e1008304	Caenorhabditis elegans
DT	21-OCT-1996	(Rel. 49, Created)
DT	01-MAR-1997	(Rel. 51, last updated, Version 5)
DE	Caenorhabditis elegans cosmid T2308	
DE	cd63 antigen like; Drosophila tissue polarity protein like;	
KW	histone H2A; histone H4; Mouse bright protein like;	
KW	transporter protein.	
KW	Eukaryota; mitochondrial eukaryotes; Metazoa; Nematoda;	
OS	Eukaryota; Rhabditida; Rhabditoidea; Secernentea; Rhabditida; Rhabditina; Rhabditoidae;	
OC		
OC		

[1]  
1-34576  
[1] d A :

Submitted (21-OCT-1996) to the EMBL/GenBank/DBJ databases.  
Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10  
1RE, England and Department of Genetics, Washington University, St.  
Louis, MO 63110, USA. E-mail: [jessanger.ac.uk](mailto:jessanger.ac.uk) or  
[rwnematode.wustl.edu](mailto:rwnematode.wustl.edu)

BASE COUNT	299	a	662	c	566	q	385	t
ORIGIN								
Query Match	7.1%	Score	52	DB	90	Length	1912;	
Best Local Similarity	39.3%	Pred. No.	2.64e-06;					
Matches	118;	Conservative	41;	Mismatches	138;	Indels	3;	Gaps 2;
bb	224	tcccgctgtgcacgcacatgcgccttacaaccatcatgcceaccatctttggacaca	283					
yy	140	TNCARYNTTCYCAYGNAATNGARTAYCARAATATGTYGTYTCNNAYTAYTNGCNY	199					
bb	284	cgaaccaaggacgcggccctggagggtcatcaattacccgtgtggaaatgtggcgt	343					
yy	200	ARAGNATGARGNNTNGARCGGGNGCNGATGATNCNYTNTGATGARCAART	259					
bb	344	gtctggccggatggccgtgtccatgtacgttcgtgtggcgggg-tg--c	400					
yy	260	GYCAYCNGAYACTAAARATTTYTTGMSNTTGYCNCNTGTYTNGAYGAYY	319					
bb	401	tggccggccatccgcctgtggccgtccatgtggaaacgcgcgcacaaaggccgggg	460					
yy	320	TNGAYGARACRATNCARCCNTGCAWSNTTGYCTNGARGTNAARGMNTGCGNC	379					
bb	461	cgctcatggaaacgttgggttcgtggccgtggccgtggccgtggccatccccc	520					
yy	380	CGNATGAGSGCCTTGYCTGCTTCCNTGCGTNGARTGAYGMENTTCNC	439					



Release 3.1A John F. Collins, Biocomputing Research Unit.  
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MSrCh\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Oct 22 15:50:45 1998: MasPar time 9.06 Seconds  
817.121 Million cell updates/sec

Tabular output not generated.

Title: >US-08-848-439-2  
Description: (1-205) from US08848439.bep  
Perfect Score: 2234

Sequence: 1 MLCGPSSLILLFLASHCCIG.....WQKGQREFKRISRSIRKQLC 295

Scoring table: PAM 150  
Gap 11

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot35  
1\_swissi

Statistics: Mean 46.742; Variance 71.562; scale 0.653

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
1	332	14.9	581	1	FRIZ_DROME	FRIZZLED PROTEIN PRECU	9.66e-53	
2	14.8	6.6	581	1	NET2_CHICK	NETRIN-2 PRECURSOR (FR	8.1e-11	
3	12.4	5.6	606	1	NET1_CHICK	NETRIN-1 PRECURSOR	3.0e-06	
4	10.9	4.9	465	1	YK18_CAEEL	HYPOTHETICAL 53.8 KD P	1.3e-03	
5	10.5	4.7	500	1	CPD4_RAT	CYTOCHROME P450 IID4 (	6.1e-03	
6	10.5	4.7	500	1	CPD1_RAT	CYTOCHROME P450 IID18	6.13e-03	
7	10.1	4.5	1741	1	RPC1_CHI	DNA-DIRECTED RNA POLIM	2.7e-02	
8	9.9	4.4	1724	1	KS61_MOUSE	RSOMSOMAL PROTEIN S6 K	5.67e-02	
9	9.8	4.4	1032	1	VG07_BPT4	BASEPLATE STRUCTURAL P	8.13e-02	
10	9.6	4.3	520	1	T0N3_CARAU	INTERMEDIATE FILAMENT	1.66e-01	
11	9.4	4.2	531	1	UD13_RAT	UDP-GLUCURONOSYLTRANSFER	3.39e-01	
12	9.2	4.1	1562	1	YMB1_YEAST	HYPOTHETICAL 180.2 KD	6.66e-01	
13	9.0	4.0	216	1	GRB_ACIS3	DNA GYrase SUBUNIT B (	1.3e+00	
14	8.9	4.0	262	1	VIRF_SHIDY	VIRULENCE REGULON TRAN	1.8e+00	
15	9.0	4.0	263	1	KSGA_MYCPN	DIMETHYLADENOSEINE TRAN	1.31e+00	
16	9.0	4.0	561	1	VTA_MAIZE	VACUOLAR AP SYNTHASE	1.8e+00	
17	8.9	4.0	752	1	KS6A_CHICK	RSOMSOMAL PROTEIN S6 K	1.8e+00	
18	8.8	3.9	127	1	YBU9_YEAST	HYPOTHETICAL 14.8 KD P	2.55e+00	
19	8.8	3.9	182	1	ILP2_CAEEL	HYPOTHETICAL 20.1 KD P	2.55e+00	
20	8.8	3.9	443	1	AM2A_ORYSA	ALPHA-AMYLASE ISOCYME	2.55e+00	
21	8.8	3.9	445	1	AMC2_ORYSA	ALPHA-AMYLASE ISOCYME	2.55e+00	
22	8.7	3.9	446	1	YHE2_SEA	HYPOTHETICAL 50.0 KD P	3.53e+00	
23	8.7	3.9	510	1	NOA1_HUMAN	ONCONEURAL VENTRAL ANT	3.53e+00	

#### ALIGNMENTS

RESULT ID	FRIZ_DROME	STANDARD; PRT;	581 AA.
AC	P18137;		
DT	01-NOV-1990 (REL. 16, CREATED)		
DT	01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)		
DT	01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)		
DE	FRIZZLED PROTEIN PRECURSOR.		
GN	FZ.		
OS	DROSOPHILA MELANOGASTER (FRUIT FLY).		
OC	EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.		
RN	[1]		
RA	SEQUENCE FROM N.A. (CLASS I).		
RA	SEQUENCE FROM N.A. (CLASS I).		
RA	MEDLINE; 8915415.		
RA	VINSON C.R.; CONOVER S.; ADLER P.N.;		
RL	NATURE 338:263-264 (1989).		
RN	[2]		
RP	SEQUENCE FROM N.A. (CLASSES I AND II).		
RX	ADLER P.N.; VINSON C.; PARK W.J.; CONOVER S.; KLEIN L.;		
RN	RNA		
RA	SEQUENCE FROM N.A. (CLASS I).		
RA	MEDLINE; 8915415.		
RA	VINSON C.R.; CONOVER S.; ADLER P.N.;		
RL	NATURE 338:263-264 (1989).		
RN	[2]		
RP	SEQUENCE FROM N.A. (CLASSES I AND II).		
RX	ADLER P.N.; VINSON C.; PARK W.J.; CONOVER S.; KLEIN L.;		
RN	RNA		
RA	SEQUENCE FROM N.A. (CLASS I).		
RA	MEDLINE; 8915415.		
RA	VINSON C.R.; CONOVER S.; ADLER P.N.;		
RL	NATURE 338:263-264 (1989).		
RN	[2]		
CC	DE FRIZZLED PROTEIN PRECURSOR.		
CC	DE FZ.		
CC	DE FZ IS REQUIRED FOR THE TRANSMISSION OF POLARITY INFORMATION, AND		
CC	DE TRANSDUCTION.		
CC	DE -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		
CC	DE -1- ALTERNATIVE PRODUCTS: CLASS I AND CLASS II PROTEINS DIFFER AT THE C-TERMINAL FROM AA 406 DUE TO USE OF ALTERNATIVE 3' EXONS.		
CC	DE EMBL: X54648; G804979;		
DR	DE DR EMBL: X54649; G804979;		
DR	DE DR EMBL: X54650; G804979;		
DR	DE DR EMBL: X54651; G804979;		
DR	DE DR EMBL: X54652; G804979;		
DR	DE DR EMBL: X54653; G804979;		
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DR			

FT	TRANSMEM	422	439	POTENTIAL.	FT	DISULFID	453	521	BY SIMILARITY.	
FT	TRANSMEM	472	492	POTENTIAL.	FT	DISULFID	468	578	BY SIMILARITY.	
FT	TRANSMEM	530	553	POTENTIAL.	FT	CARBONYD	88	88	POTENTIAL.	
FT	VAREPLIC	406	415	DILSGVCFVG -> MYLWQHTIN (IN CLASS II).	FT	CARBONYD	103	103	POTENTIAL.	
FT	VAREPLIC	416	581	MISSING (IN CLASS II).	FT	CARBONYD	394	394	POTENTIAL.	
SQ	SEQUENCE	581 AA;	64847 MW;	279885 CRC32;	FT	CARBONYD	540	540	POTENTIAL.	
Query Match		14.98;	Score 332;	DB 1; Length 581;	SQ	SEQUENCE	581 AA;	65106 MW;	5B6D2272 CRC32;	
Best Local Similarity	37.5%	Score 332;	DB 1; Length 581;		Query Match	6.68;	Score 148;	DB 1; Length 581;		
Matches	22;	Mismatches 47;	Indels 6;	Gaps 6;	Best Local Similarity	27.08;	Pred. No. 8 14e-11;			
Db	50 HNRCEBPI-T-ISICKNPNMTIMPNTNLIGHTKQEEAGLEVHQFAPLVIKGCSDDIQLQFLC 107				Matches	28;	Mismatches 46;	Indels 7;	Gaps 6;	
Qy	37 RSNCKPKIPANQLQHIGIEYQNMRLPNLGHETMKELEYQAGAWIPLVMKQCHPDTKKFLC 96				Db	431 IPIAINTSLVSTE-APADDPSYCKPAKGNYKINMKYKCKDYYVQVNILEMETVANWAK 489				
Db	108 SLYVPCV-TITLERPPIPPCRSLCSESARV-CEKLKTYNNENPENLCSKFPVYHGGSDLCLVA 165				Qy	153 IPIASSDHLIPATEAPKVCIA-CRNKNDDNDINETLCKNDFAKIVKVEITYNNDTK 211				
Qy	97 SIAFPVCLDDDDLETTIQPHCSLQVQVKDRCAFPVMSAFGFPWMDLCDRFP-QD-NDLCIP 154				Db	490 PTINILS-VVKCRDERVKR-GDNFLWIKLKDLSCKCPK1-QISKKYLVMG 536				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; OCALIFORMES.				Qy	212 IILETRSKTIVKLNGYSERDLEKKSVLWLK-DSLQCTCEMNDINAPYLVMG 261				
RN	[1]				RN	[1]				
RP	SEQUENCE FROM N.A.				RP	SEQUENCE FROM N.A.				
RC	STRAIN=WHITE LEGHORN; TISSUE=EMBRYONIC BRAIN;				RC	STRAIN=WHITE LEGHORN; TISSUE=EMBRYONIC BRAIN;				
Q90873;	MEDLINE: 94340732.				RX	MEDLINE: 94340732.				
AC	01-NOV-1987 (REL. 35, CREATED)				DT	01-NOV-1997 (REL. 35, CREATED)				
DT	01-NOV-1987 (REL. 35, LAST SEQUENCE UPDATE)				DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)				
DT	01-NOV-1987 (REL. 35, LAST ANNOTATION UPDATE)				DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	NETIN-2 PRECURSOR (FRAGMENT).				DE	NETRIN-1 PRECURSOR.				
OS	GALLUS GALLUS (CHICKEN).				OS	GALLUS GALLUS (CHICKEN).				
RA	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; OCALIFORMES.				RA	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; OCALIFORMES.				
RA	SEQUENCE FROM N.A.				RN	[1]				
RC	STRAIN=WHITE LEGHORN; TISSUE=EMBRYONIC BRAIN;				RP	SEQUENCE FROM N.A.				
Q90873;	MEDLINE: 94340732.				RC	STRAIN=WHITE LEGHORN; TISSUE=EMBRYONIC BRAIN;				
AC	01-NOV-1987 (REL. 35, CREATED)				RX	MEDLINE: 94340732.				
DT	01-NOV-1987 (REL. 35, LAST SEQUENCE UPDATE)				RA	SERAFINI T., KENNEDY T.E., GALKO M.J., MIRZAYAN C., JESSELL T.M., TESSIER-LAVIGNE M.,				
DT	01-NOV-1987 (REL. 35, LAST ANNOTATION UPDATE)				RA	TESSIER-LAVIGNE M.,				
DE	NETIN-2 PRECURSOR (FRAGMENT).				RL	CELL 78:409-424 (1994).				
CC	-1- FUNCTION: NEURINS CONTROL GUIDANCE OF CNS COMMISSURAL AXONS AND PERIPHERAL MOTOR AXONS.				CC	-1- FUNCTION: NEURINS CONTROL GUIDANCE OF CNS COMMISSURAL AXONS AND PERIPHERAL MOTOR AXONS.				
CC	-1- SUBCELLULAR LOCATION: EXTRACELLULAR.				CC	-1- SUBCELLULAR LOCATION: EXTRACELLULAR.				
CC	-1- SIMILARITY: CONTAINS ONE LAMININ N-TERMINAL DOMAIN (DOMAIN VI).				CC	-1- SIMILARITY: CONTAINS ONE LAMININ N-TERMINAL DOMAIN (DOMAIN VI).				
CC	-1- SIMILARITY: CONTAINS ONE C345C DOMAIN.				CC	-1- SIMILARITY: CONTAINS 3 LAMININ EGF-LIKE DOMAINS.				
CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				CC	-1- SIMILARITY: CONTAINS 3 LAMININ EGF-LIKE DOMAINS.				
CC	EMBL: L34550; G529421; -.				CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
DR	PROSITE: PS00022; EGF 1-2.				CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
DR	PROSITE: PS01248; LAMININ_TYPE_EGF; 3.				CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
KW	GLYCOPEPTIDE; EXTRACELLULAR MATRIX; SIGNAL; LAMININ EGF-LIKE DOMAIN; REPEAT.				CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
KW	NON-TER	1	1	POTENTIAL.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	SIGNAL	<1	15	NETRIN-1.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	CHAIN	16	581	LAMININ N-TERMINAL (DOMAIN VI).	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DOMAIN	16	261	3 X LAMININ EGF-LIKE REPEATS (LAMININ DOMAIN V-LIKE).	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DOMAIN	262	430	LAMININ EGF-LIKE 1.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DOMAIN	262	317	LAMININ EGF-LIKE 2.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DOMAIN	318	380	LAMININ EGF-LIKE 3.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DOMAIN	381	430	C345C (DOMAIN C).	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DOMAIN	431	581	CELL ATTACHMENT SITE (POTENTIAL).	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	SITE	507	509	CELL ATTACHMENT SITE (POTENTIAL).	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DISULFID	91	124	BY SIMILARITY.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DISULFID	262	271	BY SIMILARITY.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DISULFID	264	281	BY SIMILARITY.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DISULFID	283	292	BY SIMILARITY.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DISULFID	295	315	BY SIMILARITY.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DISULFID	318	327	BY SIMILARITY.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DISULFID	320	345	BY SIMILARITY.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DISULFID	348	357	BY SIMILARITY.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DISULFID	360	378	BY SIMILARITY.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DISULFID	381	393	BY SIMILARITY.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DISULFID	383	400	BY SIMILARITY.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DISULFID	402	411	BY SIMILARITY.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				
FT	DISULFID	414	428	BY SIMILARITY.	CC	-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN.				



SQ	SEQUENCE	500 AA;	56683 MW;	F01949B5 CRC32;	MUS MUSCULUS (MOUSE); CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
	Query Match	4.7%;	Score 105;	DB 1;	Length 500;
	Best Local Similarity	24.7%;	Pred. No. 6.13e-03;		
	Matches 18;	Conservative 28;	Mismatches 21;	Indels 6;	Gaps 5;
Db	160	ARCLCAAFADHSGFPFS-PNTLIDKAVNVIASLLFACR-FEYNDPREFIRLL--DLLKDT 215			OS OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
Qy	15	SHC-CLG-SARGLFLPQDFSTYKRSNCNPAPANQLCIGEYONMRFLPNLGHETMKVY 72			OC EUKARYOTA; RODENTIA.
Db	216	LEEESGFLPMLLN 228			RN [1]
Qy	73	LEQAGAWIPLVMK 85			RP SEQUENCE FROM N.A.
	RESULT	7			RX MEDLINE; 89384612.
	ID	RPC1_G1ALA	STANDARD;	PRT;	RA ALCORTA D.A.; CREWS C.M.; SWEET L.J.; BANKSTON L.; JONES S.W.;
	AC	P2202;			RA ERIKSON R.L.;
	DT	01-MAY-1992 (REL. 22, CREATED)			RL MOL. CELL. BIOL. 9:3850-3859 (1989).
	DT	01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)			CC -1- FUNCTION: PHOSPHORYLATES A WIDE RANGE OF SUBSTRATES INCLUDING
	DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			CC CC -1- RIBOSOMAL PROTEIN S6.
	DE	DE-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT (EC 2.7.7.6).			CC -1- TISSUE SPECIFICITY: INTESTINE, THYMUS, AND LUNG.
	GN	RPOA3.			CC -1- SIMILARITY: THE N-TERMINUS SHOWS HIGH SEQUENCE SIMILARITY TO THE
	OS	GIARDIA LAMBIA (GIARDIA INTESTINALIS).			CC REGIONS OF PROTEIN KINASE C, THE CATALYTIC SUBUNIT OF CAMP-DEPENDENT PROTEIN KINASE, AND CGMP-DEPENDENT PROTEIN KINASE. THE
	OC	PROTOZOA; SARCOMASTIGOPHORA; MASTIGOPHORA; DIPLOMONADIDA;			CC REMAINDER OF S6 KINASE II SHOWS HIGH SEQUENCE SIMILARITY TO THE
	RN	HEXAMITIDAE.			CC CATALYTIC SUBUNIT OF PHOSPHORYLASE B KINASE.
	RP	SEQUENCE FROM N.A.			CC EMBL; M28489; G556122; -.
	RC	STRAINS-SSP. P1;			DR PIR; B32571; B32571.
	RX	MEDLINE; 921958223.			DR HSSP; P0513; RPS6KAI.
	RA	LANZENDOERFER M.; PALM P.; GRAMPP B.; PEATTIE D.A.; ZILLIG W.;			DR MGI; MGI:104558; RPS6KAI.
	RL	NUCLEIC ACIDS RES. 20:1145-1145 (1992).			DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 2.
	CC	-1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.			DR PROSITE; PS0108; PROTEIN_KINASE_DOM; 2.
	CC	-1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE + RNA(N).			DR PROSITE; PS50011; PROTEIN_KINASE; 2.
	CC	-1- SUBUNIT: RNA POLYMERASE III CONSISTS OF ABOUT 15 DIFFERENT SUBUNITS. THIS SUBUNIT IS THE LARGEST COMPONENT OF RNA POLYMERASE III.			DR TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;
	CC	-1- SUBCELLULAR LOCATION: NUCLEAR.			DR REPEAT; MULTIGENE FAMILY.
	CC	-1- THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE mRNA PRECURSOR, AND POLYMERASE III FOR 5S rRNA.			DR DOMAIN 62 310 PROTEIN_KINASE 1.
	DR	EMBL: X60325; G9364; -			FT DOMAIN 407 664 PROTEIN_KINASE 2.
	KW	DNA-DIRECTED RNA POLYMERASE; TRANSCRIPTION; ZINC; ZINC-FINGER;			FT NP-BIND 68 76 ATP (BY SIMILARITY).
	KW	NUCLEAR PROTEIN.			FT BINDING 94 94 ATP (BY SIMILARITY).
	FT	ZN FING 79	92	C2H2-TYPE (POTENTIAL).	FT ACT-SITE 187 187 BY SIMILARITY.
	SEQ	SEQUENCE 1741 AA;	193928 MW;	DCDCD942 CRC32;	FT NP-BIND 413 421 ATP (BY SIMILARITY).
					FT BINDING 436 436 ATP (BY SIMILARITY).
					FT ACT-SITE 524 524 BY SIMILARITY.
					FT SEQUENCE 724 AA; 81594 MW; F961A261 CRC32;
					Query Match 4 48; Score 99; DB 1; Length 724;
					Best Local Similarity 35.3%; Pred. No. 5.67e-02; Indels 4; Gaps 4;
					Matches 19; Conservative 13; Mismatches 18; Indels 4; Gaps 4;
					RESULTS 9 STANDARD; PRT; 1032 AA.
	ID	VG07_BPT4			AC P19061; V1
	AC				DT 01-NOV-1990 (REL. 16, CREATED)
	DT				DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
	DT				DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
	DE				DE BASEPLATE STRUCTURAL PROTEIN GP7.
	GN				7. OS BACTERIOPHAGE T4.
	OC				OC VIRIDAE; DS-DNA NONENVELOPED VIRUSES; MYOVIRIDAE.
	RN				RN [1]
	RP				RP SEQUENCE FROM N.A.
	RC				RC STRAIN-D.
	RX				RX MEDLINE; 90384864.
	RA				RA EFIMOV V.P.; PRILIPOV A.G.; MESYANZHINOV V.V.;
	RL				RL NUCLEIC ACIDS RES. 18:5313-5313 (1990).
	CC				CC -1- FUNCTION: STRUCTURAL COMPONENT OF THE BASEPLATE.
	DR				DR EMBL: X15323; -.
	DR				DR PIR; JQ0557; G7BPT4.
	KW				KW STRUCTURAL PROTEIN.
	SEQ				SEQURE 1032 AA; 119214 MW; 39F5B2D1 CRC32;
					Query Match 4 44; Score 98; DB 1; Length 1032;
					Best Local Similarity 39.0%; Pred. No. 8.13e-02; Indels 2; Gaps 2;
	Db	368	MDSTCDKYLEALIGEVETLNANPRTSKII-DSADKGIVYN 407		Db 368 MDSTCDKYLEALIGEVETLNANPRTSKII-DSADKGIVYN 407
	QY	188	TICKNDALKIVKVEITYINRDTKILLET-KS-KTIVKLNGVSERDLKKSVLWKLDSLQC 245		QY 188 TICKNDALKIVKVEITYINRDTKILLET-KS-KTIVKLNGVSERDLKKSVLWKLDSLQC 245
	Db	226	L-QKVPEDQYI 237		QY 246 TCEEMNDINAPYL 258
	Qy				QY 246 TCEEMNDINAPYL 258
	RESULT	8	STANDARD;	PRT;	724 AA.
	ID	KS61_MOUSE			AC P18653; V1
	AC				DT 01-NOV-1990 (REL. 16, CREATED)
	DT				DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
	DT				DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
	DE				DE RIBOSOMAL PROTEIN S6 KINASE II ALPHA 1 (EC 2.7.1.-) (S6KII-ALPHA)
	GN				GN (P90-RSK1) OR RSK1.

Qy 186 METLCKNDFAALKI-KVKEITYINRDTKILETKSTKTIYKLN 225

RESULT 10  
 ID ION3\_CARAU STANDARD; PRT; 520 AA.  
 AC P18520;  
 DT 01-NOV-1990 (REL. 16, CREATED)  
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE INTERMEDIATE FILAMENT PROTEIN ON3.  
 OS EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: PISCES: GNATHOSTOMATA: OSTEICHTHYES: ACTINOPTERYGII: CYPRINIFORMES.  
 [1]  
 RN SEQUENCE FROM N. A.  
 RC TISSUE-GLIAL CELL;  
 RX MEDLINE; 90189470.  
 RA GIORDANO S.; GLASSGOW E.; TESSER P.; SCHECHTER N.; NEURON 2: 1507-1516(1989).  
 RL PIR; JS0291; JS0291.  
 PROTEIN; PS00226; IF; 1.  
 KW INTERMEDIATE FILAMENT; COILED COIL; HEPTAD REPEAT PATTERN; VISION.  
 CC FILAMENT PROTEINS OF THE VISUAL PATHWAY.  
 CC -1 SIMILARITY: SIGNIFICANT HOMOLOGY WITH MAMMALIAN TYPE II KERATIN K8.  
 CC DR NOT\_ANNOTATED\_CDS.  
 DR PIR; JS0291; JS0291.  
 PROTEIN; PS00226; IF; 1.  
 KW INTERMEDIATE FILAMENT; COILED COIL; HEPTAD REPEAT PATTERN; VISION.  
 FT DOMAIN 1 108 HEAD.  
 FT DOMAIN 109 420 ROD.  
 FT DOMAIN 421 520 TAIL.  
 FT DOMAIN 109 144 COIL 1A.  
 FT DOMAIN 145 253 COIL 1B.  
 FT DOMAIN 158 254 273 LINKER 1.  
 FT DOMAIN 274 420 420 COIL 2.  
 SQ SEQUENCE 520 AA; 57789 MW; 3E9CC03 CRC32;

Query Match 4 3%; Score 96; DB 1; Length 520;  
 Best Local Similarity 32.2%; Pred. No. 1.66e-01;  
 Matches 19; Conservative 14; Mismatches 24; Indels 2; Gaps 2;

Db 194 KINKYDEIN-KRTECENDFVLKKDVDEAMNKVELEAKLELSDEINFLRQIFEEIR 251  
 Qy 176 KRNDDNDIMETLCKNDFAALKI-KVKEITYINR-DTKILETKSTKTIYKLN 233

Query Match 4 3%; Score 96; DB 1; Length 520;  
 Best Local Similarity 32.2%; Pred. No. 1.66e-01;  
 Matches 19; Conservative 14; Mismatches 24; Indels 2; Gaps 2;

Db 194 KINKYDEIN-KRTECENDFVLKKDVDEAMNKVELEAKLELSDEINFLRQIFEEIR 251  
 Qy 176 KRNDDNDIMETLCKNDFAALKI-KVKEITYINR-DTKILETKSTKTIYKLN 233

RESULT 11  
 ID UPD13\_RAT STANDARD; PRT; 531 AA.  
 AC Q61637;  
 DT 01-NOV-1997 (REL. 35, CREATED)  
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE (UDPGT) (UGT1\*3) (UGT1\*3) (UGT1-03) (UGT1A3) (B3).  
 GN UGT1.  
 RA RATTUS NORVEGICUS (RAT).  
 OS EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA: RODENTIA.  
 RN SEQUENCE OF 1-286 FROM N. A.  
 RC STRAIN-WISTAR;  
 RX MEDLINE: 95332265.  
 RA EMI Y.; IKUSHIRO S. I.; IYANAGI T.; J. BIOPHARM. 117:392-399(1995).  
 RN SEQUENCE OF 287-531 FROM N. A.  
 RC TISSUE-LIVER;  
 RX MEDLINE: 90274676.  
 RA SATO H.; KOIWA O.; TANABE K.; KASHIWANATA S.; BIOCHEM. BIOPHYS. RES. COMMUN. 169:1260-264(1990).  
 CC -1 FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOGENOUS COMPOUNDS.

CC -1 CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCORONOSIDE; SUBCELLULAR LOCATION: MICROSONAL.  
 CC -1 ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT UDPGT ISOTYPES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
 CC -1 SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 DR EMBL; D38067; G940422; ALT-TERM.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW MULTIGENE FAMILY; MICROSONE; ALTERNATIVE SPLICING.  
 FT SIGNAL 1 25 POTENTIAL.  
 FT CHAIN 26 531 UDP-GLUCURONOSYLTRANSFERASE 1-3.  
 FT TRANSMEM 489 505 POTENTIAL.  
 FT CARBOHYD 116 116 POTENTIAL.  
 FT CARBOHYD 139 139 POTENTIAL.  
 FT CARBOHYD 293 293 POTENTIAL.  
 FT CARBOHYD 431 431 POTENTIAL.  
 SQ SEQUENCE 531 AA; 60140 MW; C3B2A846 CRC32;

Query Match 4 24%; Score 94; DB 1; Length 531;  
 Best Local Similarity 35.7%; Pred. No. 3.35e-01;  
 Matches 15; Conservative 15; Mismatches 7; Indels 5; Gaps 5;

Db 214 PVP-WNLCH-VNYGSLARLDSLQREVSVEILRHASYWL 253  
 Qy 42 PIPANOLQCHGLEYNM-RLP-NLLGHE-TMKEVLEQAGAWI 80

RESULT 12  
 ID YMB81 YEAST STANDARD; PRT; 1562 AA.  
 AC Q04791; Q04029;  
 DT 01-NOV-1997 (REL. 35, CREATED)  
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-H07 INTERGENIC REGION.  
 GN YMR247C OR YMR9408.09C OR YMR9920.01C.  
 OS SACCAROMYCES CEREVISIAE (BAKER'S YEAST).  
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.  
 RN SEQUENCE OF 1-956 FROM N. A.  
 RP STRAIN-S288C / AB972;  
 RC SUBMITTED (MAR 1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN SEQUENCE OF 1-956 FROM N. A.  
 RP STRAIN-S288C / AB972;  
 RC SUBMITTED (MAR 1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN SEQUENCE OF 950-1562 FROM N. A.  
 RP STRAIN-S288C / AB972;  
 RC GENTILES S.; BOWMAN S.; BARRELL B.G.; RAJANDREAM M.A.; WALSH S.V.; RA SUBMITTED (MAR 1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RL DR Z48539; G73295; -.  
 DR Z48756; G736313; -.  
 KW HYPOOTHETICAL PROTEIN.  
 SQ SEQUENCE 1562 AA; 180185 MW; CEE45672 CRC32;

Query Match 4 1%; Score 92; DB 1; Length 1562;  
 Best Local Similarity 38.8%; Pred. No. 6.68e-01;  
 Matches 19; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

Db 1397 KNEFDIDINSKMDRITSNDDALTIKLNNTNEVKASYLDDQKLETSFL 1445  
 Qy 176 KNKNDNDNDIMETLCKNDFAALKI-KVKEITYINR-DTKILETKSTKTIYKL 224

RESULT 13  
 ID GYRB\_AC13 STANDARD; PRT; 216 AA.  
 AC Q44273; Q00168;  
 DT 01-NOV-1997 (REL. 35, CREATED)  
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE DNA GYRASE SUBUNIT B (EC 5.99.1.3) (FRAGMENTS).  
 GN GYRB.  
 OS ACINETOBACTER SP. (STRAIN ATCC 17924 / CIP 70.12).

OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;  
 OC NEISSERIAEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97/088939;  
 RA YAMAMOTO S.; HARAYAMA S.;  
 RL INT. J. SYST. BACTERIOL. 46:506-511(1996).  
 CC -!- FUNCTION: DNA GYrase negatively supercoils closed circular double-stranded DNA in an ATP-dependent manner and also catalyzes the interconversion of other topological isomers of double-stranded DNA rings, including catenanes and knotted rings.  
 CC -!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING OF DOUBLE-STRANDED DNA.  
 CC -!- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE ENZYME FORMS AN A2B2 TETRAMER.  
 DR EMBL; D73436; G1322101; -.  
 DR PROSITE; PS00177; TOPOISOMERASE-II; 1;  
 DR TOPOISOMERASE; ISOMERASE; ATP-BINDING; ANTIBIOTIC RESISTANCE.  
 KW NON\_TER 1  
 FT NON\_CONS 116 117  
 FT NON\_TER 216 216  
 SQ SEQUENCE 216 AA: 23775 MW: E572EEEO CRC32;

RESULT 14  
 ID VIRF\_SHIDY STANDARD: PRT; 262 AA.  
 AC 004218;  
 DT 01-JUN-1994 (REL 29, CREATED)  
 DT 01-JUN-1994 (REL 29, LAST SEQUENCE UPDATE)  
 DE VIRULENCE REGULON TRANSCRIPTIONAL ACTIVATOR VIRF.  
 GN SHIGELLA DYSENTERIAE, SHIGELLA FLEXNERI, AND SHIGELLA SONNEI.  
 OG PLASMID 210 KB INVASION.  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 OC ENTEROBACTERIACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA SPECIES=S-DYSENTERIAE; STRAIN=CG97;  
 RA YAO R.; REDDY L.V.; PALCHAUDHURI S.;  
 RL SUBMITTED (MAR-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S-FLEXNERI; STRAIN=2A;  
 RX MEDLINE; 87032409;  
 RA SAKAI T.; SASAKAWA C.; MAKINO S.; YOSHIKAWA M.;  
 RL INFECT. IMMUN. 54:395-402(1986).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S-SONNEI;  
 RX MEDLINE; 89212881;  
 RA KATO J. I.; ITO K. I.; NAKAMURA A.; WATANABE H.;  
 RL INFECT. IMMUN. 57:1391-1398(1989).  
 RN [4]  
 RP SIMILARITY TO ARAC FAMILY.  
 RX MEDLINE; 92326642.  
 RA DORMAN C.J.;  
 RL MOL. MICROBIOL. 6:1575-1575(1992).  
 CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF THE VIRB GENE WHICH IS

CC -!- ITSELF AN ACTIVATOR OF THE IPAABCD VIRULENCE REGULON.  
 CC -!- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL REGULATORS.  
 CC EMBL; X58464; G44954; -.  
 DR EMBL; M29177; G152801; -.  
 DR EMBL; X16661; G41067; -.  
 DR PIR; S14646; S14646; -.  
 DR PIR; A47605; A47605.  
 DR PROSITE; PS00041; HTH\_ARAC\_FAMILY-1; 1.  
 DR PROSITE; PS01124; HTH\_ARAC\_FAMILY-2; 1.  
 KW PLASMID; VIRULENCE; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING.  
 FT DNA\_BIND 177 196 H-T-H MOTIF (BY SIMILARITY).  
 SQ SEQUENCE 262 AA: 30549 MW: 11339838 CRC32;

Query Match 4.0%; Score 89; DB 1; Length 262;  
 Best Local Similarity 25.5%; Pred. No. 1.3e+00;  
 Matches 13; Conservative 21; Mismatches 15; Indels 2; Gaps 2;

Db 37 TLTIDEGQIAFERNIONINVSIKSIDSINPFFIISLDNLNSIIRIMEPI 87  
 Qy 195 ALKIVKVEITYINRDKILLETK-SKTIYKLNGVS-ERDLKKSVLWLKDSDL 243

RESULT 15  
 ID KSGA\_MYCPN STANDARD: PRT; 263 AA.  
 AC P75113; -.  
 DT 01-NOV-1997 (REL 35, CREATED)  
 DT 01-NOV-1997 (REL 35, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL 35, LAST ANNOTATION UPDATE)  
 DE DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-) (S-ADENOSYL METHIONINE-6'-N', DE (N6-ADENOSYL RNA) DIMETHYLTRANSFERASE) (16S RNA DIMETHYLTRANSFERASE) (HIGH DE LEVEL KASUGAMYCIN RESISTANCE PROTEIN KSGA) (KASUGAMYCIN DE DIMETHYLTRANSFERASE).  
 DE KSGA.  
 OS MYCOPLASMA PNEUMONIAE.  
 OC PROKARYOTA; Tenericutes; Mollicutes; Mycoplasma; Mycoplasmatales;  
 OC Mycoplasmataceae.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 29342 / M129;  
 RX MEDLINE; 97105885;  
 RA HIMMELREICH R.; HILBERTH H.; PLAGENS H.; PIRKL E.; LI B.; -C., RA HERRMANN R.;  
 RL NUCLEIC ACIDS RES. 24:4420-4449(1996).  
 CC -!- FUNCTION: SPECIFICALLY DIMETHYLATES TWO ADJACENT ADENOSINES IN THE LOOP OF A CONSERVED HAIRPIN NEAR THE 3'-END OF 16S RNA IN THE 30S PARTICLE. ITS INACTIVATION LEADS TO KASUGAMYCIN RESISTANCE (BY SIMILARITY).  
 CC -!- SIMILARITY: STRONG, TO OTHER BACTERIAL KSGA.  
 CC -!- SIMILARITY: BELONGS TO THE RNA ADENINE N-6-METHYLTRANSFERASE FAMILY.  
 CC EMBL; AE000017; G1673824; -.  
 DR PROSITE; PS01131; RNA\_A\_DIMETH; 1.  
 DR MRNA PROCESSING; TRANSFERASE; METHYLTRANSFERASE;  
 KW MRNA PROCESSING; TRANSFERASE; METHYLTRANSFERASE;  
 RN [2]  
 CC ANTIBIOTIC RESISTANCE.  
 SQ SEQUENCE 263 AA: 29794 MW: 357400D CRC32;

Query Match 4.0%; Score 90; DB 1; Length 263;  
 Best Local Similarity 37.0%; Pred. No. 1.31e+00;  
 Matches 20; Conservative 11; Mismatches 20; Indels 3; Gaps 3;

Db 52 KLOQPVHIGIELDKRILAEYLWNLLEEQLTIGDQLNQDQFDTIPILGC 104  
 Qy 46 NIQL-CHGIEQNMRLPN-LIGHETNKEVLEQAGAWIPLYMKQCHDDTKKFLCS 97

Search completed: Thu Oct 22 15:51:11 1998  
 Job time : 26 secs.



ACCESSIONS S78444  
 REFERENCE  
 #authors Bhanot, P.; Wang, Y.; Nathans, J.  
 #submission submitted to the EMBL Data Library, July 1996  
 #accession S78444  
 #status preliminary  
 #molecule-type DNA  
 #residues 1-694 #label BHA  
 #crosses-references EMBL:U65589  
 SUMMARY #length 694 #molecular-weight 75437 #checksum 3113  
 Query Match 15.9%; Score 355; DB 2; Length 694;  
 Best Local Similarity 36.2%; Pred. No. 2.44e-46;  
 Matches 47; Conservative 32; Mismatches 45; Indels 6; Gaps 6;  
 Db 51 YGVPAIP-KDPNLRCEETIPCRGIGNMITSFPNENHETDEAGLEVHQFW-PLVEIK 1.08  
 Qy 28 FGQPDSEYKRSNCKPPANLQLCHGIEYQNMRLPNLGHMETKEV-LEQAGAWIPLYMKQ 86  
 Db 109 CSPDLKFLCSMWTPIKLEDYHKLPVCRSVERARSGCAPTMQOYSFEWPERMACEHLP 1.68  
 Qy 87 CHPDTKFLCSFAPVCLDDLETIQFCHSLCQVKDRCAPIVSAFGEFPWPDMLECDRFP 146  
 Db 169 LHGDPDNLCM 1.78  
 Qy 147 -Q-D-NDLCI 153

RESULT 3  
 ENTRY S71786 #type complete  
 TITLE df22\_protein - fruit fly (Drosophila melanogaster)  
 ORGANISM #formal\_name Drosophila melanogaster  
 DATE 12-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change  
 ACCESSIONS S71786  
 REFERENCE  
 #authors Bhanot, P.; Brink, M.; Harryman-Sanos, C.; Hsieh, J.C.; Wang, Y.; Mackie, J.P.; Andrew, D.; Nathans, J.; Nusse, R.  
 #journal Nature (1996) 382:225-230  
 #title A new member of the frizzled family from Drosophila functions as a wingless receptor.  
 #accession S71786  
 #status preliminary; nucleic acid sequence not shown  
 #molecule-type DNA  
 #residues 1-694 #label BHA  
 #crosses-references EMBL:U65589  
 SUMMARY #length 694 #molecular-weight 75423 #checksum 3095  
 Query Match 15.9%; Score 355; DB 2; Length 694;  
 Best Local Similarity 36.2%; Pred. No. 2.44e-46;  
 Matches 47; Conservative 32; Mismatches 45; Indels 6; Gaps 6; Gaps 6;  
 Db 51 YGVPAIP-KDPNLRCEETIPCRGIGNMITSFPNENHETDEAGLEVHQFW-PLVEIK 1.08  
 Qy 28 FGQPDSEYKRSNCKPPANLQLCHGIEYQNMRLPNLGHMETKEV-LEQAGAWIPLYMKQ 86  
 Db 109 CSPDLKFLCSMWTPIKLEDYHKLPVCRSVERARSGCAPTMQOYSFEWPERMACEHLP 1.68  
 Qy 87 CHPDTKFLCSFAPVCLDDLETIQFCHSLCQVKDRCAPIVSAFGEFPWPDMLECDRFP 146  
 Db 169 LHGDPDNLCM 1.78  
 Qy 147 -Q-D-NDLCI 153

RESULT 4  
 ENTRY S15709 #type complete  
 TITLE hypothetical protein - fruit fly (Drosophila melanogaster)  
 ORGANISM #formal\_name Drosophila melanogaster  
 DATE 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change  
 ACCESSIONS S15709  
 REFERENCE

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RESULT 3  
 ENTRY S71786 #type complete  
 TITLE df22\_protein - fruit fly (Drosophila melanogaster)  
 ORGANISM #formal\_name Drosophila melanogaster  
 DATE 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change  
 ACCESSIONS S03540  
 REFERENCE  
 #authors Vinson, C.R.; Conover, S.; Adler, P.N.  
 #journal Nature (1989) 338:265-264  
 #title A Drosophila tissue polarity locus encodes a protein containing seven potential transmembrane domains.  
 #accession S03540  
 #status not compared with conceptual translation  
 #molecule-type mRNA  
 #residues 1-581 #label VIN  
 REFERENCE S15708  
 #authors Adler, P.N.; Vinson, C.; Park, W.J.; Conover, S.; Klein, L.  
 #journal Genetics (1990) 126:401-416  
 #title  
 #molecular structure of frizzled, a Drosophila tissue polarity gene.  
 #crosses-references EMBL:91060073  
 #accession S15708  
 #status preliminary  
 #molecule-type DNA  
 #crosses-references EMBL:U54648  
 GENETICS  
 #genes FlyBase:fz  
 #crosses-references FlyBase:FBgn0001085  
 #introns 224/3; 264/3; 329/3; 405/1  
 FEATURE 1-26 #domain signal sequence #status predicted #label SIG\\  
 27-381 #product gene frizzled protein #status predicted #label MAT  
 SUMMARY #length 581 #molecular-weight 64846 #checksum 358  
 Query Match 14.9%; Score 332; DB 2; Length 581;  
 Best Local Similarity 37.5%; Pred. No. 8.11e-42;  
 Matches 45; Conservative 22; Mismatches 47; Indels 6; Gaps 6;

Db	50	HNRCEIT-T-1SCKNTPYNNNTIMPLNLIGHTQEEAGLEHVQAPALVIGCSDDQDQLQLCLC	107
Qy	37	RSNCKEIPANQLQCHGEYQNNRQLPNLIGHTEMKEVLEQAGAWIPLMKQCHPTDKFLC	96
Db	108	SLYVPC-TILERPIPPCRSLICESARV-CEKLMTKVNENWPENLCSKFPVHGDEDIYVA	165
Qy	97	SLFAPVCLDDDETQCHSLCQVQKDRCAPVMSAFCGPWPDMLCEDRFP-OD-NDLCIP	154
RESULT	6		
ENTRY		B56101 #type fragment	
TITLE		collagen alpha 1(XVIII) chain precursor long form - mouse	
ORGANISM		(fragment)	
DATE		#formal_name Mus musculus #common_name house mouse	
ACCESSION		03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change	
REFERENCE		10-Sep-1997	
REFERENCE		B56101	
REFERENCE		Rehn, M., Pihlajaniemi, T.	
REFERENCE		J. Biol. Chem. (1995) 270:4705-4711	
REFERENCE		Identification of three N-terminal ends of type XVIII	
REFERENCE		collagen chains and tissue-specific differences in the	
REFERENCE		expression of the corresponding transcripts. The longest	
REFERENCE		form contains a novel motif homologous to rat and	
REFERENCE		Drosophila frizzled proteins.	
#accession		B56101	
#molecule_type		preliminary	
#residues		1-562 #label REH	
GENETICS		#cross-references GB:011637; NID:9618429; PID:9618430	
#gene		COL18A1	
SUMMARY		#length 562 #checksum 115	
Query Match		8.0% Score 178 DB 2; Length 562;	
Best Local Similarity		34.1% Pred. No. 3-36e-13;	
Matches		30; Conservative 13; Mismatches 45; Indels 0; Gaps	
Db	368	SRCLPLPPITLCSRIGIGHFWLPHLHHTDSEVEATVQAMGRFLHTNCHPFLAWFFCLC	427
Qy	38	SNCKPPTANQLQCHGEYQNNRQLPNLIGHTEMKEVLEQAGAWIPLMKQCHPTDKFLC	97
Db	428	LLAPSSGPGPPPLPPCQRFCEALEDEC 455	
Qy	98	LFAPVCLDDDETQCHSLCQVQKDRC 125	
RESULT	7		
ENTRY		B54665 #type fragment	
TITLE		netrin-2 precursor - chicken (fragment)	
ORGANISM		#formal_name Gallus gallus #common_name chicken	
DATE		06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change	
ACCESSION		10-Sep-1997	
REFERENCE		B54665	
REFERENCE		Serfini, T.; Kennedy, T.E.; Gallo, M.J.; Mirzayan, C.;	
REFERENCE		Jessell, T.M.; Tessier-Lavigne, M.	
REFERENCE		Cell (1994) 78:409-424	
REFERENCE		The netrins define a family of axon outgrowth-promoting	
REFERENCE		proteins homologous to Caenorhabditis elegans UNC-6.	
#accession		B54665	
#molecule_type		preliminary	
#residues		1-581 #label SER	
#cross-references		GB:L34550; NID:9529420; PID:9529421	
SUMMARY		#length 581 #checksum 7731	
Query Match		6.6% Score 148 DB 2; Length 581;	
Best Local Similarity		27.0% Pred. No. 3-23e-08;	
Matches		30; Conservative 28; Mismatches 46; Indels 7; Gaps	
Db	431	IPAINNTSLVTSIE-APADCDSYCKPAKGNYKINMMKYCKKDVYVQNLNETVYANAK	489

QY	153	IPASSDHILLPATEAPKYPEA-CRKNKDDNDIMETLCKNDFAKKVKEITYINRDTK	211
Db	490	FTN1L5-VYKCRDPERVKR-GDNFLWILHKDLSCKCPK1-QISKKVLYMG	536
	:	::	:
QY	212	ILETKSKTIYKLNGYSERDLKKSVLWLK-DSLOCTCEEMNDINAPLIVMG	261
RESULT	8		
ENTRY		A54665 #type complete	
TITLE		nefrin-1 precursor - chicken	
ORGANISM		#formal_name Gallus gallus #common_name chicken	
DATE		06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change	
ACCESSIONS		10-Sep-1997	
REFERENCE		A54665	
#authors		Serafini, T.; Kennedy, T.E.; Galko, M.J.; Mirzayan, C.; Jessell, T.M.; Tessier-Lavigne, M.	
#journal		Cell (1994) 78:409-424	
#title		The nefrins define a family of axon outgrowth-promoting	
		proteins homologous to Caenorhabditis elegans UNC-6.	
#accession		A54665	
###status		preliminary	
		##molecule-type mRNA	
		##residues 1-606 ##label SER	
SUMMARY		##cross-references 1-L3459; PID:9529419	
		#length 606 #molecular-weight 68126 #checksum 5400	
Query Match		Score 124; DB 2; Length 606;	
Best Local Similarity		26.1%; Pred. No. 1.57e-04;	
Matches	31	Conservative 34; Mismatches 41; Indels 13; Gaps 1	
Db	456	IPAAAPPPTAASSTEPPAD-CDSYCKASKGKLUKINMKYCKKKYAVQIHLKAEKADM-W	513
	:	::	:
QY	153	IPASSDHILLPATEAPKYPEA-CRKNKDDNDIMETLCKNDFAKKVKEITYINRDT	210
Db	514	KFTN1L5-VYK-QG-SNR-LRQDQTLYNHWAKDACKCPKVPKKK-YLLGSTD	566
	:	::	:
QY	211	KIILETTSKTIYKLNGYSERDLKKSVLWLKD-SVLOCTCEEMNDINAPLIVMG	266
RESULT	9		
ENTRY		JC5539 #type complete	
TITLE		Smoothed protein - mouse	
ORGANISM		#formal_name Mus musculus #common_name house mouse	
DATE		02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change	
ACCESSIONS		05-Sep-1997	
REFERENCE		JC5539; PC4476	
#authors		Akiyama, H.; Shigeno, C.; Hiraki, Y.; Shukunami, C.; Kohno H.; Akagi, M.; Konishi, J.; Nakamura, T.	
#journal		Biochem. Biophys. Res. Commun. (1997) 235:142-147	
#title		Cloning of a mouse Smoothed cDNA and expression patterns hedgehog signaling molecules during chondrogenesis and cartilage differentiation in clonal mouse EC cells, ATDC	
#accession		JC5539	
###molecule-type mRNA			
#accession		#residues 1-793 ##label AKI	
#accession		PC4476	
###molecule-type protein		528-533-539-545; 600-605 ##label AK2	
COMMENT		##experimental_source ADTC5 cell	
		This protein is used in the conserved targets in Hedgehog signalling pathway, together with Patched and Gli. These proteins are responsible for the skeletal abnormalities in Gorlin and Greig syndromes.	
FEATURE		5.5% #domain signal sequence #status Predicted #label SIG	
1-32		#length 793 #molecular-weight 87299 #checksum 8609	
SUMMARY		Query Match Best Local Similarity 2.7%; Pred. No. 3.30e-04; Mismatches 22; Conservative 31; Indels 9; Gaps	



QY 246 TCEEMNDINAPYL 258

RESULT 13 H6425 #type complete  
ENTRY hypothetical protein b0872 - Escherichia coli (strain K-12)  
TITLE #formal\_name Escherichia coli  
ORGANISM 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change  
DATE 14-Nov-1997

ACCESSIONS H64835

REFERENCE A64730

#authors Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Bullard, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Roe, C.R.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, Y.

#journal Science (1997) 277:1453-1462

#title The complete genome sequence of Escherichia coli K-12.

#cross-references MUID:97426617  
accession H64835

#status preliminary; nucleic acid sequence not shown;  
translation not shown

##molecule\_type DNA

##residues 1-322 ##label BLAT

##cross-references GB:AE000189; GB:000096; PID:91787098;

URCP:bs0872

##experimental\_source strain K-12, Substrain MG1655  
SUMMARY #length 322 #molecular-weight 35740 #checksum 5190

Query Match 4.4%; Score 99; DB 2; Length 322;  
Best Local Similarity 27.5%; Pred. No. 5.25e-01;  
Matches 19; Conservative 22; Mismatches 21; Indels 7; Gaps 7;

Db 87 RDVKRGDYLWLSDAMGEPCTCDKAE-DK-FLLLAA-GCGVTPPMSMRFLAKRQADYR 143  
Qy 230 RDLKKSV-LWLDKL-QCTCEMDINAPYLNGQKQGELVITSVKRM-QRGOREFK-R 285

Db 144 VIXNVRTPQ 152  
Qy 286 ISRSIRKLQ 294

RESULT 14 E64474 #type complete  
ENTRY hypothetical protein MJ1398 - Methanococcus jannaschii  
TITLE #formal\_name Methanococcus jannaschii  
ORGANISM 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change  
DATE 10-Oct-1997

ACCESSIONS E64474

REFERENCE A64300

#authors Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.A.; Fitzgerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.; Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scott, J.L.; Geoghegan, N.S.M.; Weidman, J.F.; Fuhrmann, J.D.; Nguyen, D.; Utterback, T.R.; Kelley, J.M.; Peterson, K.M.; Hurst, M.A.; Hanna, M.C.; Cotton, M.D.; Roberts, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.

#journal Science (1996) 273:1058-1073

#title Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.

#cross-references MUID:96337999  
accession E64474

#status preliminary; nucleic acid sequence not shown;  
translation not shown

##molecule\_type DNA

##residues 1-391 ##label BUL

##cross-references GB:U67580; GB:L77117; NID:91592044; PID:91592046;  
TIGR:MTJ398; PID:91511417

GENETICS #map\_position FOR1358185-1359160

SUMMARY #length 391 #molecular-weight 45529 #checksum 6984

Query Match 4.4%; Score 98; DB 2; Length 391;  
Best Local Similarity 30.0%; Pred. No. 7.08e-01;  
Matches 15; Conservative 19; Mismatches 14; Indels 2; Gaps 2;

Db 84 LRFKTEKNSVNLITTKVNTNKAIFTSTINGSBVGNGNTIWIKDPL 133  
Qy 196 LKIKVETIYINRDKIILETKSKTI-YKLNGVSERDILKKS-VLMKLDSL 243

RESULT 15 B32571 #type complete  
ENTRY ribosomal protein S6 kinase II (EC 2.7.-.) alpha chain  
TITLE homolog (Clone MuFA) - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change  
26-Feb-1998

ACCESSIONS B32571

REFERENCE Alcorta, D.A.; Crews, C.M.; Sweet, L.J.; Bankston, L.; Jones, S.W.; Erikson, R.L.

#authors Mol. Cell. Biol. (1989) 9:3850-3859

#journal Sequence and expression of chicken and mouse rsk: homologs of Xenopus laevis ribosomal S6 kinase.

#cross-references MUID:89384612

##molecule\_type mRNA

##residues 1-724 ##label ALC

##cross-references GB:M23489

CLASSIFICATION #superfamily ribosomal protein S6 kinase II; protein kinase homology

KEYWORDS ATP; phosphotransferase; serine/threonine-specific protein kinase

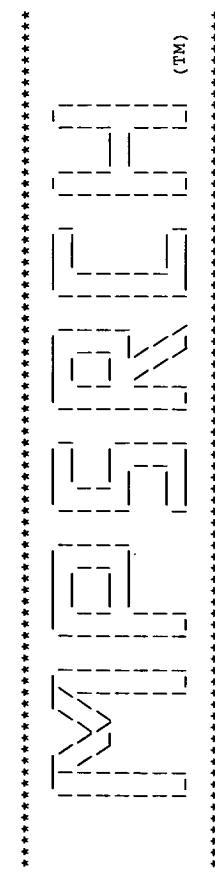
FEATURE B32571 #domain protein kinase homology #label KIN1  
#region protein kinase ATP-binding motif  
#domain protein kinase homology #label KIN2

SUMMARY #length 724 #molecular-weight 81594 #checksum 4206

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Best Local Similarity 35.2%; Pred. No. 5.25e-01;  
Matches 19; Conservative 13; Mismatches 18; Indels 4; Gaps 4;

Db 489 KI-LRQKFEBREASFVLTISKIVETLHSQGVWARDLRSFSNLLYVDESGNPEC 541  
Qy 197 KIKVETIYINRDKIILETKSKTI-YKLNGVSERDILKKS-VLMKLDSLQCTC 247

Search completed: Thu Oct 22 15:54:26 1998  
Job time : 72 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Oct 22 15:57:27 1998: MasPar time 17.59 Seconds

tabular output not generated.

Title: >US-08-848-439-3

Description (1-25) from US8848439.pep

Perfect Score: 2073

Sequence: 1 SARGSLFLGQDPDSYKRSRNC.....WQKGOREFRRKRSRIRKLOC 275

Scoring table: PAM 150  
Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: sptrembl6

1:sp\_archaea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human  
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc  
9:sp\_phage 10:sp\_plant 11:sp Rodent 12:sp\_unclassified  
13:sp\_virus 14:sp\_virus

Statistics: Mean 44.690; Variance 72.884; scale 0.613

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	Pred. No.	-----
1	2067	99.7	295 11	008862	SECRETED FRIZZLED RELA	0.00e+00	-----	
2	2065	99.6	295 11	035297	SECRETED APOPOSIIS REL	0.00e+00	-----	
3	2062	99.5	295 11	P97299	STROMAL CELL DERIVED F	0.00e+00	-----	
4	1377	66.4	206 4	014778	SECRETED APOPOSIIS REL	0.00e+00	-----	
5	913	44.0	314 4	014779	SECRETED APOPOSIIS REL	3.00e-193	-----	
6	911	43.9	313 4	000546	SECRETED FRIZZLED-RELA	9.94e-193	-----	
7	901	43.5	308 6	019116	FRZA PRECURSOR	1.94e-190	-----	
8	890	42.9	317 4	014780	SECRETED APOPOSIIS REL	3.42e-190	-----	
9	729	35.2	314 11	008861	SECRETED FRIZZLED RELA	2.10e-187	-----	
10	582	28.1	307 13	042397	CRESCENT	8.17e-147	-----	
11	398	19.2	281 13	073821	SECRETED XWNT8 INHIBIT	3.03e-110	-----	
12	396	19.1	568 5	016147	MOM-5.	1.38e-65	-----	
13	394	19.0	592 13	057328	7-TRANSMEMBRANE PROTEI	2.38e-65	-----	
14	396	19.1	572 11	061090	FRIZZLED HOMOLOG 7 (TR	4.11e-65	-----	
15	394	19.0	591 4	000144	FRIZZLED HOMOLOG 7	1.23e-64	-----	
16	394	18.9	685 11	061091	FRIZZLED HOMOLOG 8 (TR	1.23e-64	-----	
17	391	18.9	567 13	057329	7-TRANSMEMBRANE PROTEI	6.31e-64	-----	
18	392	18.9	626 11	070421	FRIZZLED-1.	3.65e-64	-----	
19	386	18.6	565 4	Q14332	FRIZZLED GENE PRODUCT.	9.65e-63	-----	
20	386	18.6	570 11	Q08464	FRIZZLED PROTEIN HOMOL	9.65e-63	-----	

#### ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	295 AA.
ID	008862			
AC	008862;			
DT	01-JUL-1997 (TREMBREL. 04, CREATED)			
DT	01-JUL-1997 (TREMBREL. 04, LAST SEQUENCE UPDATE)			
DT	01-JUN-1998 (TREMBREL. 06, LAST ANNOTATION UPDATE)			
DE	SECRETED FRIZZLED RELATED PROTEIN SFRP-2.			
GN	SFRP2.			
OS	MUS MUSCULUS (MOUSE).			
OC	EUCARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 97250455.			
RA	RATTNER A., HSIEH J.C., SMALLWOOD P.M., GILBERT D.J., COPELAND N.G.,			
RA	JENKINS N.A., NATHANS J.			
RL	PROC. NATL. ACAD. SCI. U.S.A. 94:2859-2863 (1997).			
DR	EMBL: U88567; G1946343; -.			
SO	SEQUENCE 295 AA; 33469 MW; 23680DDA CRC32;			
Query	Match	99.78;	Score 2067;	DB 11; Length 295;
Best Local	Similarity 99.3%;	Pred. No. 0.00e+00;	1; Mismatches 0;	Indels 0; Gaps 0;
Matches	273;	Conservative	1;	

21 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

22 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

23 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

24 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

25 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

26 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

27 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

28 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

29 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

30 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

31 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

32 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

33 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

34 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

35 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

36 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

37 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

38 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

39 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

40 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

41 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

42 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

43 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

44 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

45 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

46 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

47 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

48 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

49 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

50 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

51 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

52 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

53 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

54 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

55 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

56 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

57 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

58 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

59 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

60 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

61 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

62 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

63 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

64 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

65 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

66 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

67 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

68 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

69 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

70 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

71 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

72 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

73 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

74 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

75 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

76 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

77 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

78 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

79 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

80 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

81 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

82 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

83 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

84 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

85 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

86 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

87 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

88 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

89 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

90 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

91 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

92 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

93 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

94 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

95 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

96 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

97 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

98 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

99 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

100 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

101 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

102 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

103 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

104 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

105 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

106 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

107 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

108 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

109 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

110 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

111 SARGSLFLGQDPDSYKRSRNCPIKAPNLQQLHGIEYQNMQLPNLIGHTMKVLEQAGAWI 80

RESULT 2	PRELIMINARY;	PRT;	295 AA.	
ID 035297				
AC P97299				
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)				
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)				
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)				
DE SECRETED APOPTOSIS RELATED PROTEIN 1.				
GN SARPI.				
OS MUS.MUSCULUS (MOUSE).				
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC EUTHERIA; RODENTIA.				
RN [1]				
RP SEQUENCE FROM N.A.				
RA MELKONYAN H., CHIANG W.C., SHAPIRO J.P., MAHADEVAPPA M.,				
RA FITZPATRICK P.A., KIEFFER M.C., TOMEI D.L., UMANSKY S.R.,				
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.				
DR EMBL; AF01989; G241521; -.				
SEQUENCE 295 AA; 33483 MW; 0E4C8ABE CRC32;				
RESULT 4	PRELIMINARY;	PRT;	206 AA.	
ID 014778				
AC Q14778				
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)				
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)				
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)				
DE SECRETED APOPTOSIS RELATED PROTEIN 1 (FRAGMENT).				
GN SARPI.				
OS HOMO SAPIENS (HUMAN).				
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC EUKARYOTA; PRIMATES.				
RN [1]				
RP SEQUENCE FROM N.A.				
RA FITZPATRICK H., CHANG W.C., SHAPIRO J.P., MAHADEVAPPA M.,				
RA FITZPATRICK P.A., KIEFFER M.C., TOMEI D.L., UMANSKY S.R.,				
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.				
DR EMBL; AF01796; G241515; -.				
FT NON-TER 206				
SQ SEQUENCE 206 AA; 23215 MW; F465B6B CRC32;				
Query Match 99.6%; Score 2065; DB 11; Length 295;				
Best Local Similarity 98.9%; Pred. No. 0.00e+00;				
Matches 272; Conservative 2; Mismatches 1; Indels 0; Gaps 0;				
Db 21 SARGELFLFGOPDFSYKRTNCKPPIPANQLQCHIEQYQMRPLNLGHETMKEYLEQAGAWI 80				
Qy 1 SARGELFLFGOPDFSYKRSNCKPPIPANQLQCHIEQYQMRPLNLGHETMKEYLEQAGAWI 60				
Db 81 PLVMKQCHPDKFLCSLFPCLDDLETIOPCHSCLVQYDRCAPVMSA_GFPPWDFML 1.40				
Qy 61 PLVMKQCHPDKFLCSLFPCLDDLETIOPCHSCLVQYDRCAPVMSA_GFPPWDFML 1.20				
Db 141 ECDREFPONDLCIPLASSDHLIUPATEEAPKYECAECKTCKNEDNDIMETLCKNDFAKIKV 200				
Qy 121 ECDREFPONDLCIPLASSDHLIUPATEEAPKYECAECKNNDNDIMETLCKNDFAKIKV 180				
Db 201 KEITYINRDTKILEKSKT1KLYNGSERDCKSVLWKLDSLQCTCEEMNDINAPYLM 260				
Qy 181 KEITYINRDTKILEKSKT1KLYNGSERDCKSVLWKLDSLQCTCEEMNDINAPYLM 240				
Db 261 GQKQGELVITSVKRQNGKQRBFKRISRSIRKLQC 295				
Qy 241 GQKQGELVITSVKRQNGKQRBFKRISRSIRKLQC 275				
RESULT 3	PRELIMINARY;	PRT;	295 AA.	
ID P97299				
AC P97299				
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)				
DT 01-JUN-1998 (TREMBLREL. 03, LAST SEQUENCE UPDATE)				
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)				
DE STROMAL CELL DERIVED FACTOR 5 (SDF5) 5				
GN SDF5.				
OS MUS.MUSCULUS (MOUSE).				
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC EUTHERIA; RODENTIA.				
RN [1]				
RP SEQUENCE FROM N.A.				
RX MEDLINE; 97092816.				
RA SHIROZU M., TADA H., TASHIRO K., NAKAMURA T., LOPEZ N.D., NAZAREA M.,				
RA HAMADA T., SATO T., NAKANO T., HONJO T.,				
DR GENOMICS; 37:273-280 (1996).				
DR MGD; MG1:108078; SDF5.				
SEQUENCE 295 AA; 33501 MW; 32988C8 CRC32;				
Query Match 99.5%; Score 2062; DB 11; Length 295;				
Best Local Similarity 98.9%; Pred. No. 0.00e+00;				
Matches 272; Conservative 2; Mismatches 1; Indels 0; Gaps 0;				
Db 21 SARGELFLFGOPDFSYKRSNCKPPIPANQLQCHIEQYQMRPLNLGHETMKEYLEQAGAWI 80				
Qy 1 SARGELFLFGOPDFSYKRSNCKPPIPANQLQCHIEQYQMRPLNLGHETMKEYLEQAGAWI 60				
RESULT 5	PRELIMINARY;	PRT;	314 AA.	
ID 014779				
AC Q14779				
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)				
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)				
DE SECRETED APOPTOSIS RELATED PROTEIN 2.				
GN SDF2.				
OS HOMO SAPIENS (HUMAN).				
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC EUKARYOTA; PRIMATES.				
RN [1]				
RP TISSUE=HEART;				
RC TISSUE=HEART;				

RA	MELKONYAN H., PROCHAZKA V., CHANG W. C., UMANSKY S. R.;	Db	283 IHKWDKKNKEFKNMKKMKHNHEC 305
DR	SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBBJ DATA BANKS.	AC	019116; PRELIMINARY; PRT; 308 AA.
SQ	SEQUENCE 314 AA; 35411 MW; 61E26155 CRC32;	DT	01-JAN-1998 (TREMBLREL. 05, CREATED)
		DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
		DT	01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
		DE	FRZA PRECURSOR.
		OS	OS TAURUS (BOVINE).
		OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
		OC	EUTHERIA; ARTIODACTyla.
		RN	SEQUENCE FROM N.A.
		RP	TISSUE=HEART;
		RC	RA SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBBJ DATA BANKS.
		RL	DR EMBL; U85945; G2337937; -.
		KW	SIGNAL.
		FT	POTENTIAL.
		SQ	SEQUENCE 308 AA; 34763 MW; 9B/4A92F CRC32;
			Query Match 43 %; Score 902; DB 6; Length 308;
			Best Local Similarity 42 %; Pred. No. 1.91e-190;
			Matches 111; Conservative 66; Mismatches 79; Indels 7; Gaps 5;
		Db	45 FYTRPPQCVIDIPADLRLCHNYGKKMVLPNLLEHETMAEVKQASSWPLNKNCIGTQ 104
		AC	13 FSYKRSNCKPIAPNLQCHGIEYQNMRLPNLQGHETMKEVLEQNGAWITLVMKQCHPDTK 72
		DT	01-JUL-1997 (TREMBLREL. 04, CREATED)
		DT	01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
		DT	01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
		DE	SECRETED FRIZLED-RELATED PROTEIN.
		OS	OS SAPTENS (HUMAN).
		OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
		OC	EUTHERIA; PRIMATES.
		RN	SEQUENCE FROM N.A.
		RP	TISSUE=JUNG;
		RA	FINCH P. W., HE X., KELLEY M. J., UREN A., SCHAUDES R. P., POPESCU N. C.,
		RA	RUDIKOFF S., ARONSON S. A., VARNUS H. F., RUBIN J. S.;
		RJL	SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBBJ DATA BANKS.
		RN	[2]
		RP	SEQUENCE FROM N.A.
		RA	ZHOU Z., WANG J.;
		RJL	SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBBJ DATA BANKS.
		DR	DR EMBL; AF001900; G221389; -.
		DR	DR EMBL; AF056087; G303351; -.
		SQ	SEQUENCE 313 AA; 35314 MW; A3CD04FF CRC32;
			Query Match 43.9%; Score 911; DB 4; Length 313;
			Best Local Similarity 42.6%; Pred. No. 9.94e-193;
			Matches 112; Conservative 67; Indels 7; Gaps 5;
		Db	50 FYTKPPQCVIDIPADLRLCHNYGKKMVLPNLLEHETMAEVKQASSWPLNKNCIGTQ 109
		AC	13 FSYKRSNCKPIAPNLQCHGIEYQNMRLPNLQGHETMKEVLEQNGAWITLVMKQCHPDTK 72
		DT	01-JUL-1997 (TREMBLREL. 04, CREATED)
		DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
		DT	01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
		DE	SECRETED APOPTOSIS RELATED PROTEIN 3.
		GN	GN SAPTENS (HUMAN).
		OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
		OC	EUTHERIA; PRIMATES.
		RN	SEQUENCE FROM N.A.
		RP	TISSUE=PANCREAS;
		RC	MELKONYAN H., CHANG W. C., SHAPIRO J. P., MAHADEVAPPA M.;
		RA	RA FITPATRICK P. A., KIEFER M. C., TOMEI D. L., UMANSKY S. R.;
		RA	RA SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBBJ DATA BANKS.
		DR	DR AF017988; G2415419; -.
		DR	DR SEQUENCE 317 AA; 35577 MW; 2CD69373 CRC32;
			Query Match 43 %; Score 901; DB 4; Length 317;
			Best Local Similarity 45.2%; Pred. No. 3.42e-190;

Matches	114;	Conservative	58;	Mismatches	74;	Indels	6;	Gaps	4;
Db	46	SYSKPQCLDIPADLPLCHTYGKMRMLPNULEHESLAEVKQASSWLPILLKCRHSDTQ	105						
Qy	14	SY-KRSNCKTPANIQLQCHGLEYQNMRLPNLGHETMKEYQAWIPLYMKOCHPDTK	72						
Db	106	VFCLSLFAPVCLD--RPIYPCRSLEAVRAGCAPLMEAYGPWPENLCHRFPLDNDLC	162						
Qy	73	KFCLSLFAPVCLDDETIOPCHSLCQVQRDCAPTMASAFGPWPDMLECDFPQONDLC	132						
Db	163	IAYQFG-HLPATAPPVTKIACQ-EMEHSADGLMEOMCSSDEFVVKRRIKEIENGDRKL	220						
Qy	133	IPASSDHLPATEAPKVEACKNQFNDNIDMETLCKNDALKVKEYTINYRDTKI	192						
Db	221	IGAQKKKKLKKPGLPKRKDKTKRVLHMKGNGCPCPQLDSLAGSFYMGKVDGQLLMA	280						
Qy	193	IELEKSKTIYKLNGYSERDLKKSVLWLKDSTQCTCBEMNDINAPLYMGQKGGELVITS	252						
Db	281	YRNDQKKNEMK	292						
Qy	253	VKRQKGQREBFK	264						
RESULT 9									
Db	008861;	PRELIMINARY;	PRT;	314	AA.				
Qy	01-JUL-1997	(TREMBLREL. 04, CREATED)							
Db	01-JUL-1997	(TREMBLREL. 04, LAST SEQUENCE UPDATE)							
Qy	01-JUN-1998	(TREMBLREL. 06, LAST ANNOTATION UPDATE)							
Db	SECRETED FRIZZLED RELATED PROTEIN SFRP-1.								
Qy	SFRP-1.								
Db	MUS MUSCULUS (MOUSE).								
Qy	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;								
Db	EUTHERIA; RODENTIA.								
Qy	[1] SEQUENCE FROM N.A.								
Db	RELINE, 97250455.								
Qy	RATTNER, A., HSEIEH, J.C., SMALLWOOD, P.M., GILBERT, D.J., COPELAND, N.G.,								
Db	JENKINS, N.A., NATHANS, J.J.,								
Qy	PROC. NATL. ACAD. SCI. U.S.A. 94:2859-2863 (1997).								
Db	01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)								
Qy	01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)								
Db	SECRETED FRIZZLED RELATED PROTEIN SFRP-1.								
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Db	SECRETED FRIZZLED RELATED PRO								

Qy	17	RSNCRPIPANIQLQCHGIEYQNMRLPNLIGHETMKVELEQAGAWIPLVMKQCHPDTKFLC	76
Db	125	SMYAPYC-TVLEQALPPCRSLCERARQCEALMNKEGFQWPDTRCEKFVHGAEIYCYG	183
Qy	77	SLFAPCQLDDDETIPQCHSLCQVQVKDRCAVPMASFGEFPWDDMLECRFP-QDN-DLICIP	134
Db	184	QNASERGTPT	193
Qy	135	LAASSDHILPA	144
<b>RESULT 14</b>			
ID	Q61090	PRELIMINARY;	PRT;
AC	Q61090;		572 AA.
DT	01-NOV-1996	(TREMBLRL. 01, CREATED)	
DT	01-NOV-1996	(TREMBLRL. 01, LAST SEQUENCE UPDATE)	
DT	01-JAN-1998	(TREMBLRL. 05, LAST ANNOTATION UPDATE)	
DE	FIZZLED HOMOLOG 7	(TRANSMEMBRANE RECEPTOR).	
GN	FZD7 OR FRIZZLED 7.		
OS	MUS MUSCULUS (MOUSE)		
OC	EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; RODENTIA.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE; 95224032.		
RA	WANG Y., MACKE J.P., ABELLA B. S., ANDREASSON K., WORLEY P. ,		
RA	GILBERT D.J., COPELAND N.G., JENKINS N.A., NATHANS J. ;		
RL	J. BIOL. CHEM. 271:4468-4476 (1996).		
DR	U43320; G115128; -.		
DR	MGI: 108570; FZD7.		
KW	TRANSMEMBRANE		
SQ	SEQUENCE 572 AA;	63816 MW;	FA1D78D2 CRC32;
<b>Query Match 14</b>			
Best Local Similarity	19.1%	Score 396;	DB 11;
Matches	48;	Length 572;	Length 572;
Best Local Similarity	40.7%	Pred. No. 4.1le-65;	
Matches	25;	Mismatches 42;	Indels 3; Gaps
<b>RESULT 15</b>			
ID	Q00144	PRELIMINARY;	PRT;
AC	Q00144;		591 AA.
DT	01-JUL-1997	(TREMBLRL. 04, CREATED)	
DT	01-JUL-1997	(TREMBLRL. 04, LAST SEQUENCE UPDATE)	
DT	01-JAN-1998	(TREMBLRL. 05, LAST ANNOTATION UPDATE)	
DE	FIZZLED HOMOLOG.		
GN	FZD3.		
OS	HOMO SAPIENS (HUMAN)		
OC	EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; PRIMATES.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE; 9722723.		
RA	WANG Y.K., HARRIMAN SAMOS C. , PEOPLES R. , PEREZ-JURADO L.A. , NUSSE R. ,		
RA	FRANCKE U. ;		
RL	HUM. MOL. GENET. 6:465-472(1997).		
DR	U82159; G1906558; -		
SQ	SEQUENCE 591 AA;	64466 MW;	88C5EC1F CRC32;
<b>Query Match 15</b>			
Best Local Similarity	19.0%	Score 394;	DB 4;
Matches	48;	Length 591;	Length 591;
Best Local Similarity	37.5%	Pred. No. 1.23e-64;	
Matches	32;	Mismatches 47;	Indels 1; Gaps
<b>RESULT 16</b>			
ID	AVEIPMCRGIGYNLTRMPNLIGHETMKVELEQAGAWIPLVMKQCHPDTKFLC	100	

Qy 24 PANLQLCHGIEYQNMRLPNLIGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVC 83  
Db 101 TDQVSTPIACRPMCQARLRCAPIMEQFNFGWPDSLDCARLPRTRNDPHALMEAPENAT 160  
Db 84 LDLDLDETIQPCPHSLCQVKDRCAPVNSAEGFPWPDMLECDRFPQDNDL-C1PLASSDHLL 142  
Db 161 AGPAEPHK 168  
Db 143 PATEEAPK 150  
Qy 143 PATEEAPK 150

Search completed: Thu Oct 22 15:58:52 1998  
Job time : 85 secs.

The logo consists of a stylized 'T' and 'M' formed by a dashed line. The 'T' is on the left, and the 'M' is on the right, with a diagonal line connecting their tops. The entire logo is enclosed in a rectangular border.

Title: >US-08-848-439-3  
Prescription: (1-275) from US08848439.pop  
Reflex Score: 2073  
Concurrent Score: 1  
1 SARGELFGOPDFSYKRSNC.....WOKGOREFKRSRSRKLOC 275

scoring table: PAM 150 Gap 11

searched: 120441 secs: 36531193 residues

post-processing: Minimum Match 0.8  
Maximum Match 0.15  
Summary of

database: **pir56**

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

## SUMMARIES

Query result

Ref. No.	Source	Accession No.	Protein Design No.	Description
1	386	18.6	641	2 A450544 probable intercellular
2	386	17.1	694	2 S78444 dfz2 protein - fruit
3	355	17.1	694	2 S71786 dfz2 protein - fruit
4	332	16.0	415	2 S15709 hypothetical protein
5	332	16.0	581	2 S03540 gene frizzled protein
6	178	8.6	562	2 B56101 collagen alpha 1(XVII)
7	148	7.1	581	2 B54665 neprin-2 precursor -
8	124	6.0	606	2 A54655 neprin-1 precursor -
9	122	5.9	793	2 JC5539 smoothed protein -
10	101	4.9	1735	2 S2812 DNA-directed RNA Poly
11	99	4.9	322	2 H64825 hypothetical protein
12	100	4.8	500	2 D31579 cytochrome P450 2D4 -
13	100	4.8	500	2 C32131 cytochrome P450 2D4 h
14	99	4.8	724	2 B32571 ribosomal protein S6
15	98	4.7	391	2 E64474 hypothetical protein
16	98	4.7	1032	1 G7BPT4 basiplate protein gp7
17	97	4.7	15281	2 S41309 cyclosporin synthetas
18	96	4.6	520	2 JS0291 intermediate filament
19	96	4.6	735	2 I51901 ribosomal Protein S6
20	94	4.5	271	2 E64694 hypothetical protein
21	93	4.5	735	2 A53300 ribosomal protein S6
22	92	4.4	203	2 B70254 conserved hypothetical
23	92	4.4	608	2 B70188 hypothetical protein

## ALIGNMENTS

```

RESULT 1
ENTRY A45054      #type complete
TITLE probable intercellular signal transducer or transmitter Fz-1
- rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway, rat
DATE 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change
28-Apr-1995
ACCESSIONS A45054
REFERENCE Chan, S.D.; Karpf, D.B.; Fowlkes, M.E.; Hooks, M.; Bradley, C.D.; M.S.; Vuong, V.; Bambino, T.; Liu, M.Y.; Arnaud, Strevier, G.J.; Nissensohn, R.A.
#journal J. Biol. Chem. (1992) 267:25202-25207
#title Two homologs of the Drosophila polarity gene frizzled ( fz )
#cross-references A45054
#accession A45054
#status preliminary; not compared with conceptual translation
#molecule_type nucleic acid
#residues 1-641 #label CNA
#experimental_source UMR 106 osteosarcoma cell line
#note sequence extracted from NCBI:1120154
#summary 41007641 #protein_id 1120154 #label CNA

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Query	Match	Score	DB	Length
HCYCOPI-S-IPCLCTDIAYNOTIMPINLLGHTNOEDAGLEYHQFYPLVKYVOCASAEKKFLC	108	386	2	641
RSNCKPIPPANLQLQHGIETQNMRLLGHTMKVELEQASAWIPLVMQCPDTKKFLC	17	105	51	6
SMYAPVC-TVLEQALPPCSLICERARG-CRALMNKFGEQWSDTLKCEKFPVHGRGELCVG	166	223	223	76
SIFPVCLQDLDLDETOQPCSHLCLCYVKDRCAFPVMSAFGEWPNDMLECDFEP-QD-NDICIP	77	134	134	134
QNTSD	228			
LASSD	139			
RESULT	2	S78444	#Type complete	
ENTRY	.	dfr2	protein - fruit fly (Drosophila melanogaster)	
TITLE		#formal_name	Drosophila melanogaster	
ORGANISM		#sequence_revision	13-Mar-1998	
DATE	12-Mar-1998	13-Mar-1998	12-Mar-1998	

ACCESSIONS S78444  
 #authors Adler, P.N.; Vinson, C.; Park, W.J.; Conover, S.; Klein, L.  
 #submission S78444  
 #status submitted to the EMBL Data Library, July 1996  
 #molecule\_type DNA  
 #residues 1-694 #label BHA  
 #cross-references EMBL:055589  
 SUMMARY #length 694 #molecular-weight 75437 #checksum 3113  
 Query Match 17.1%; Score 355; DB 2; Length 694;  
 Best Local Similarity 36.2%; Pred. No. 1.19e-45;  
 Matches 47; Conservative 32; Mismatches 45; Indels 6; Gaps 6;  
 Db 51 YGVPAIP-KDPNLRCEETIPCRGIGYNNMTSPNEMNNHETQDEAGLEVHQFW-PLVEIK 108  
 Qy 8 FGQDPSYKRSCSKTPANLQLCHGIEVNMRPLNLGHETKKEV-LEQAGAWIPLVMQ 66  
 Db 109 CSPDKEFLCSWYTPICLEDYKPLPVCRSVERASCAPIMQYSSEWPERMACBHP 168  
 Qy 67 CHPDTKFLCSFAPVCLDDDETIQFCHSLCQVRDRCAPMSAGFPPWPMLECDRFP 126  
 Db 169 LHGDPDNLCM 178  
 Qy 127 -Q-D-NDLCI 133

RESULT 3  
 ENTRY S71786 #type complete  
 TITLE df22 protein - fruit fly (Drosophila melanogaster)  
 ORGANISM #formal\_name Drosophila melanogaster  
 DATE 12-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change  
 ACCESSIONS S71786  
 REFERENCE S71786  
 #authors Bhanot, P.; Brink, M.; Harryman Santos, C.; Hsieh, J.C.; Wang, Y.; Macie, J.P.; Andrew, D.; Nathans, J.; Nusse, R.  
 #journal Nature (1996) 382:225-230  
 #title A new member of the frizzled family from Drosophila functions as a wingless receptor.  
 #accession S71786  
 #status preliminary; nucleic acid sequence not shown  
 #molecule\_type DNA  
 #residues 1-694 #label BHA  
 #cross-references EMBL:055589  
 SUMMARY #length 694 #molecular-weight 75423 #checksum 3095  
 Query Match 17.1%; Score 355; DB 2; Length 694;  
 Best Local Similarity 36.2%; Pred. No. 1.19e-45;  
 Matches 47; Conservative 32; Mismatches 45; Indels 6; Gaps 6;  
 #status preliminary; nucleic acid sequence not shown  
 #molecule\_type DNA  
 #residues 1-694 #label BHA  
 #cross-references EMBL:055589  
 SUMMARY #length 694 #molecular-weight 75437 #checksum 3113  
 Query Match 17.1%; Score 355; DB 2; Length 694;  
 Best Local Similarity 36.2%; Pred. No. 1.19e-45;  
 Matches 47; Conservative 32; Mismatches 45; Indels 6; Gaps 6;  
 Db 51 YGVPAIP-KDPNLRCEETIPCRGIGYNNMTSPNEMNNHETQDEAGLEVHQFW-PLVEIK 108  
 Qy 8 FGQDPSYKRSCSKTPANLQLCHGIEVNMRPLNLGHETKKEV-LEQAGAWIPLVMQ 66  
 Db 109 CSPDKEFLCSWYTPICLEDYKPLPVCRSVERASCAPIMQYSSEWPERMACBHP 168  
 Qy 67 CHPDTKFLCSFAPVCLDDDETIQFCHSLCQVRDRCAPMSAGFPPWPMLECDRFP 126  
 Db 169 LHGDPDNLCM 178  
 Qy 127 -Q-D-NDLCI 133

RESULT 4  
 ENTRY S15709 #type complete  
 TITLE hypothetical protein - fruit fly (Drosophila melanogaster)  
 ORGANISM #formal\_name Drosophila melanogaster  
 DATE 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change  
 ACCESSIONS S15709  
 REFERENCE

authors Adler, P.N.; Vinson, C.; Park, W.J.; Conover, S.; Klein, L.  
 journal Molecular structure of frizzled, a Drosophila tissue polarity gene.  
 accession S15709 #status preliminary  
 #molecule\_type DNA  
 #residues 1-415 #label ADL  
 #cross-references EMBL:X54648  
 GENETICS #length 581 #molecular-weight 64846 #checksum 358  
 #introms 224/3; 264/3; 329/3; 405/1  
 #product gene frizzled protein #status predicted #label SIG\\  
 #domain signal sequence #status predicted #label SIG\\  
 #introms 224/3; 264/3; 329/3; 405/1  
 #product gene frizzled protein #status predicted #label MAT  
 SUMMARY #length 581 #molecular-weight 64846 #checksum 358  
 Query Match 16.0%; Score 332; DB 2; Length 581;  
 Best Local Similarity 37.5%; Pred. No. 3.3e-41;  
 Matches 45; Conservative 22; Mismatches 47; Indels 6; Gaps 6;

Db	50	HNRCEPI-T-TSICKNTPYNTIMPNLIGHTKQEAGLEVIQFAPLVKIGSDDQFLFC 107
Qy	17	RSNCKPPIPANLQLCHTEYQNNRPLNLGHETMKVLEQAGAWIPLMKQCHPDTKKFLC 76
Db	108	SLVYPPC-TILERPIPCCRSLESARY-CERKLMTKYNENPENLCSKFPVHGGEDLCAV 165
Qy	77	SLFAPVCLDDDETQCHSLCQVQVKDRCAPVMSAEGFPWDMLECDRFP-QD-NDLCIP 134
RESULT	6	B56101 #type fragment collagen alpant 1(XVIII) chain precursor long form - mouse (fragment)
ENTRY		#formal_name Mus musculus #common_name house mouse
TITLE		03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 10-Sep-1997
ORGANISM		
DATE		
ACCESSION		B56101
REFERENCE		A56101 Rehn, M.; Pihlajaniemi, T. J. Biol. Chem. (1995) 270:4705-4711 Identification of three N-terminal ends of type XVIII collagen chains and tissue-specific differences in the expression of the corresponding transcripts. The longest form contains a novel motif homologous to rat and Drosophila frizzled proteins.
AUTHORS		
JOURNAL		
TITLE		
GENETICS		
#gene		
SUMMARY		B56101 #status preliminary #molecule_type mRNA ##residues 1-1562 ##label REH #cross-references GB:U11637; NID:9618429; PMID:9618430
COL18A1		
#length	562	#checksum 115
Query Match		8.63; Score 178; DB 2; Length 562;
Best Local Similarity		34.1%; Pred. No. 4.36e-13;
Matches	30;	Conservative 13; Mismatches 45; Indels 0; Gaps
Db	368	SRCLPPDPTLTCRSLRGIGHFWLPLHDTOSVEBATVQAWGRFLDTCHPFLFAWEFLC 427
Qy	18	SNCKKPPIPANLQLCHTEYQNNRPLNLGHETMKVLEQAGAWIPLMKQCHPDTKKFLC 77
Db	428	LLAPSCGPGPPPLPPCPCRFCEALEDEC 455
Qy	78	LFAPVCLDDDETQCHSLCQVQVKDRC 105
RESULT	7	B54665 #type fragment netrin-2 precursor - chicken (fragment)
ENTRY		#formal_name Gallus gallus #common_name chicken
TITLE		06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Sep-1997
ORGANISM		
DATE		
ACCESSION		B54665
REFERENCE		Serafini, T.; Kennedy, T.E.; Galko, M.J.; Mirzayan, C.; Jessel, T.M.; Tessier-Lavigne, M. Cell (1994) 78:409-424 The netrins define a family of axon outgrowth-promoting proteins homologous to <i>Caenorhabditis elegans</i> UNC-6.
AUTHORS		
JOURNAL		
TITLE		
GENETICS		
#gene		
SUMMARY		B54665 #status preliminary #molecule_type mRNA ##residues 1-581 ##label SER #cross-references GB:L35550; NID:9529420; PMID:9529421 #length 581 #checksum 7731
Query Match		7.1%; Score 148; DB 2; Length 581;
Best Local Similarity		27.0%; Pred. No. 4.04e-08;
Matches	30;	Conservative 28; Mismatches 46; Indels 7; Gaps
Db	431	IPAINPISLVTSTE-APADCOSYCKPKAGKNYKCKDYYVQNLLEMETANWAK 489



ENTRY I52313 #type complete  
 TITLE cytochrome P450 2D4 homolog, brain (clone 2d-29) - rat  
 ORGANISM #formal\_name: *Rattus norvegicus* #common\_name: Norway rat  
 DATE 27-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change  
 23-Jan-1998

ACCESSIONS I52313  
 REFERENCE I52313  
 #authors Kawashima, H.; Strobel, H.W.  
 Biochem. Biophys. Res. Commun. (1995) 209:535-540  
 #title CDNA Cloning of a novel rat brain cytochrome P450 belonging  
 to the CYP2D subfamily  
 #cross-references MUID:95251650  
 #accession I52313  
 #molecule\_type preliminary; translated from GB/EMBL/DDJB  
 #residues 1-500 #label RES  
 #cross-references GB: S7859; NID:998524; PID:998525  
 #experimental\_source brain, strain Sprague-Dawley  
 CLASSIFICATION #superfamily cytochrome P450  
 KEYWORDS heme; transmembrane protein  
 FEATURE heme  
 4.16 #binding\_site heme iron (Cys) (axial ligand) #status  
 Predicted  
 SUMMARY #length 500 #molecular\_weight 56683 #checksum 8540  
 Query Match 4.8%; Score 100; DB 2; Length 500;  
 Best\_Local\_Similarity 26.7%; Pred. No. 3.97e-01;  
 Matches 16; Conservative 22; Mismatches 18; Indels 4; Gaps 3;  
 Db 173 EPFS-PNTLLDKAVCNVIASLLFACR-FEYNDPRFIRLL--DLKDITLEEESGFLPMLN 228  
 Qy 6 FFLGQDPDFSYKRSNCKPAPNQLQRCIEYONRNLPNLGHETMKEYLEQAWIPLVMK 65

RESULT 14 B32571 #type complete  
 ENTRY ribosomal protein S6 kinase II (EC 2.7.-.-) alpha chain  
 TITLE homolog (clone MuA) - mouse  
 ORGANISM #formal\_name: *Mus musculus* #common\_name: house mouse  
 DATE 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change  
 26-Feb-1998

ACCESSIONS B32571  
 REFERENCE A93113  
 #authors Alcorta, D.A.; Crews, C.M.; Sweet, L.J.; Bankston, L.; Jones, S.W.; Erikson, R.L.  
 Mol. Cell. Biol. (1989) 9:3850-3859  
 #title Sequence and expression of chicken and mouse rsk: homologs of  
*Xenopus laevis* ribosomal S6 kinase.  
 #cross-references MUID:8938412  
 #accession B32571  
 #molecule\_type mRNA  
 #residues 1-724 #label ALC  
 #cross-references GB:M22489

CLASSIFICATION #superfamily ribosomal protein S6 kinase II; protein kinase homology  
 KEYWORDS ATP; phosphotransferase; serine/threonine-specific protein kinase

FEATURE 60-310 #domain protein kinase homology #label KIN1  
 68-76 #region protein kinase ATP-binding motif  
 405-664 #domain protein kinase homology #label KIN2  
 #molecular\_weight 81534 #checksum 4206

Query Match 4.8%; Score 99; DB 2; Length 724;  
 Best\_Local\_Similarity 35.2%; Pred. No. 5.34e-01;  
 Matches 19; Conservative 13; Mismatches 18; Indels 4; Gaps 4;

Db 489 KI-LRQKFFSEBEASFVLTISKTVEYLHSQGVYHRDLKPSNLYVDESGNPEC 541  
 Qy 177 KIKVKEIITYINRDTKILLETRSKTI-Y-KLNQYSERDLKKS-VLWLKDSDLQCTC 227

RESULT



RESULT ID 035297	PRELIMINARY;	PRT;	295 AA.
AC 015297;			
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)			
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)			
DE SECRETED APOPTOSIS RELATED PROTEIN 1.			
GN SARPI.			
OS MUS MUSCULUS (MOUSE)			
EUKARYOTA; METIZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC EUTHERIA; RODENTIA.			
RN [1]			
RP SEQUENCE FROM N.A.			
RA FITZPATRICK P.A., KIEFER M.C., TOMEI D.L., UMANSKY S.R.;			
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR EMBL: AF017989; G2415421; -			
SQ SEQUENCE 295 AA; 33483 MW; 0E4C8A8E CRC32;			
Query Match 97.9%; Score 2188; DB 11; Length 295;			
Best Local Similarity 97.6%; Pred. No. 0.00e+00;			
Matches 288; Conservative 4; Mismatches 3; Indels 0; Gaps 0;			
Db 1 MPRGPASLLLVLASHCCLGSGARGLFQGDPDSYKRTNCKPIPANQLQCHGIEYONMRL 60			
Qy 1 MLOQPGSLLLFLASHCCLGSGARGLFQGDPDSYRSNCPIPANQLQCHGIEYONMRL 60			
Db 61 PNLLGHETMKVEVLEQAGAWIPLVMKCHPDTKFLCSLFAPIVCLDDLETIOPCHSLCVO 120			
Qy 61 PNLLGHETMKVEVLEQAGAWIPLVMKCHPDTKFLCSLFAPIVCLDDLETIOPCHSLCVO 120			
Db 121 VKDRCAPIVMSAFIGFPMPDMLCDRFPQNDLICPLASSDHILLPATEAPIVCEACKTNE 180			
Qy 121 VKDRCAPIVMSAFIGFPMPDMLCDRFPQNDLICPLASSDHILLPATEAPIVCEACKNND 180			
Db 181 DDNDIMETLCKNDEALKIKEYITYINRDTKILETTSKTYKLNGSERDLKSVIWLK 240			
Qy 181 DDNDIMETLCKNDEALKIKEYITYINRDTKILETTSKTYKLNGSERDLKSVIWLK 240			
Db 241 DSQLCTCEEMNDINAPYLVNGQKQGELVITSVKRMQKGOREFKRISRIRKLQC 295			
Qy 241 DSQLCTCEEMNDINAPYLVNGQKQGELVITSVKRMQKGOREFKRISRIRKLQC 295			
RESULT ID P97299	PRELIMINARY;	PRT;	295 AA.
AC P97299;			
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)			
DT 01-JUN-1998 (TREMBLREL. 03, LAST SEQUENCE UPDATE)			
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)			
DE STROMAL CELL DERIVED FACTOR 5 (SDF5).			
GN SDF5.			
OS MUS MUSCULUS (MOUSE)			
EUkaryota; Metizoa; Chordata; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC EUTHERIA; RODENTIA.			
RN SEQUENCE FROM N.A.			
RP MEDLINE; 97092876.			
RA SHIROZU M., TADA H., TASHIRO K., NAKAMURA T., LOPEZ N.D., NAZAREA M., HAMADA T., SATO T., NAKANO T., HONJO T.; GENOMICS 37:27-280 (1996).			
DR EMBL: D50462; G174702; -; MGI: 108078; SDF5.			
SQ SEQUENCE 295 AA; 33501 MW; 329888C8 CRC32;			
Query Match 97.8%; Score 2185; DB 11; Length 295;			
Best Local Similarity 97.6%; Pred. No. 0.00e+00;			
Matches 288; Conservative 4; Mismatches 3; Indels 0; Gaps 0;			
Db 1 MPRGPASLLLVLASHCCLGSGARGLFQGDPDSYKRSNCPIPANQLQCHGIEYONMRL 60			
Qy 1 MLOQPGSLLLFLASHCCLGSGARGLFQGDPDSYKRSNCPIPANQLQCHGIEYONMRL 60			
RESULT ID O14779	PRELIMINARY;	PRT;	314 AA.
AC O14779;			
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)			
DT 01-AUG-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)			
DE SECRETED APOPTOSIS RELATED PROTEIN 2.			
GN SARP2.			
OS HOMO SAPIENS (HUMAN)			
OC EUKARYOTA; METIZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC EUTHERIA; PRIMATES.			
RN SEQUENCE FROM N.A.			
RC TISSUE=HEART;			



Matches	114;	Conservative	58;	Mismatches	74;	Indels	6;	Gaps	4;	DT	01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
Db	46	SYSKPPQCLDIPADLPLCITYKVRMLPMLFHESTLAEVKQOASSWPLLNKRNCHSDTQ	105							OS	GALLUS GALLUS (CHICKEN).
Qy	34	SY-KRSNCKPITANLQLCHGIEQNMRNLPNLGHETMEVLEDAWAPIYKQCHPDTK	92							OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGUTHAE;
		[1]								RN	GALLIFORMES.
Db	106	VFCLSLFAPVCLD--RPIYPCRSILCEAVRAGCAPLMEAYGFWPEMLHCKRPLDNDLC	162							RP	SEQUENCE FROM N.A.
Qy	93	KFLCSLFAPVCLDIPITQPSLCLCYQYKDRAPVNSAEGFPWPDMECDREFPQDNDLC	152							RA	SUPERFIER P. L., IZIPISSA-BELMONTE J. C., DE ROBERTIS E. M.;
		[1]								RL	SUBMITTED (MAY-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
Db	163	IAVQF-HLPATAPPVTKICAQ-EMERSADGLIMEQWCKMIREKKEIILNGDRKL	220							DR	EMBL; AF006508; G226372; -
Qy	153	IPASSDHLLPATEAKVCEACKNKKNDNIMETLCKNDALKVKEYTINYRDTKI	212							SQ	SEQUENCE 307 AA; 34883 MW; 320A2243 CRC32;
		[1]								Query Match	32.6%; Score 729; DB 13; Length 307;
Db	221	IGAQKKEKKLKKPLKPLKRDTKLVLHMKNGACGCPOLDSLASELIMGRKVTDGQJLIMA	280							Best Local Similarity	35.8%; Pred. No. 2.17e-151;
Qy	213	IELETSKTIKKLNGVSEDLKSVLWLRSLOCTCEEMNDINAPLYMGQKGGELVITS	272							Matches	96%; Conservative 68; Mismatches 94; Indels 10; Gaps 8;
Db	281	YWRNDKKNKEMK	292							Db	36 SYLRRSSCTATPRSMALCYDIGYSEMIPNLLEHETMPEVIQSSWLPULLARECHPDA
Qy	273	VKRWQKGOREFK	284							Qy	95 SY-KRSNCKPITANLQLCHGIEYQNNRNLPNLGHETMKEVLEQAGAWIPLMKQCHPDT
		[1]								Db	91 RIFLCSLAPICLDRL-TYPCRSILCEAVRAGCAPLMEAYGFWPEMLHCKRPLDNDLC
		[1]								Qy	92 KFKLCSLFAPVCLDIPITQPSLCLCYQYKDRAPVNSAEGFPWPDMECDREFPQDNL
RESULT	9	PRELIMINARY;	PRT;	314	AA.					Db	153 CTAATVSTDS-SSSSRMFRASCKDCELEASTARELIDNLCANDETYKIRLKRNTTV
ID	008861;									Qy	211 209
AC	008861;									Db	152 CIPASSHLLPATEAKV-CEACK NKKNDNDNIMETLCKNDALKVKEYTINYRDTKI
DT	01-JUL-1997	(TREMBLREL.	04,	CREATED)						Qy	209
DT	01-JUL-1997	(TREMBLREL.	04,	LAST SEQUENCE UPDATE)						Db	212 SDFDLDPSRVEYLKPGPPLRTEPGLQWQDIDATCAHNTMRGTHAGGVFVISGEVRS
DT	01-JUN-1998	(TREMBLREL.	06,	LAST ANNOTATION UPDATE)						Qy	271 SDFDLDPSRVEYLKPGPPLRTEPGLQWQDIDATCAHNTMRGTHAGGVFVISGEVRS
DE	SECRETED FRIZZLED RELATED PROTEIN SFRP-1.									Db	210 TKILETRSKTIKKLNGVSEDLKSVLWLRSLOCTCEEMNDINAPLYMGQKGG
GN	SFRP1.									Qy	267 XWNT8 INHIBITOR SIZZLED.
OS	MUS MUSCULUS (MOUSE).									Db	272 VVNNKAYAWQKKNRNLHQAVRWRKHHRC
EUKARYOTA;	METAZOA;	CHORDATA;	VERTEBRATA;	TETRAPODA;	MAMMALIA;					Qy	299 268 LVTSVKKWQKGOREFKRSRSRKLQG
OC	EUTHERIA;	RODENTIA.									
RN	[1]										
RP											
SEQUENCE FROM N.A.											
RA	JATTER N. A., HSIEH J. C., SMALLWOOD P. M., GILBERT D. J., COPELAND N. G.,										
RA	JENKINS N. A., NATHANS J.,										
RL	PROC. NATL. ACAD. SCI. U.S.A. 94:2859-2863(1997).										
DR	U88566; GI:194634; -.										
SQ	SEQUENCE 314 AA; 35327 MW; 5AA5CA27 CRC32;										
Query Match	39.8%; Score 890; DB 11; Length 314;										
Best Local Similarity	41.4%; Pred. No. 2.76e-193;										
Matches	109; Conservative 67; Mismatches 80; Indels 7; Gaps 5;										
Db	51	FYTKPPQCVDFYDVLRLCHNYGKMMVLPNLLEHETMAEVKQOASSWPLLNKRNCHMGTQ	110							RESULT	11
Qy	33	FSYKRSNCKPITANLQLCHGIEQNMRNLPNLGHETMEVLEQAVIPLMKQCHPDTK	92							ID	073821;
		[1]								AC	073821;
Db	111	VFCLSLFAPVCLD--RPIYPCRSILCEAVRAGCAPLMEAYGFWPEMLHCKRPLDNDLC	166							DT	01-AUG-1998 (TREMBLREL. 07, CREATED)
Qy	93	KFLCSLFAPVCLDIPITQPSLCLCYQYKDRAPVNSAEGFPWPDMECDREFPQDNDLC	152							DT	01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
		[1]								DT	01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
Db	167	IAMTPPNTTEASKPQGKDNELKSEA-LIEHLCASEFALVLEKMKIKEYKENGDKKI	225							DE	SECRETED XWNT8 INHIBITOR SIZZLED.
Qy	153	IPASSDHLLPATEAKVCEACKNKKNDNIMETLCKNDALKVKEYTINYRDTKI	212							GN	SZL
		[1]								OS	XENOPUS LAEVIS (AFRICAN CLAWED FROG).
Db	226	V-PKKKKPL-KIGPIKKKELAKALVLELKNGADCPCPCHOLDNLSEHNLIMGRKVQKSYQYLTA	283							RN	XENOPUS LAEVIS (AFRICAN CLAWED FROG).
Qy	213	IELETSKTIKKLNGVSEDLKSVLWLRSLOCTCEEMNDINAPLYMGQKGGELVITS	272							RP	SEQUENCE FROM N.A.
Db	284	IHKWDKKNEKEPNFNEWMRMKHNC	306							RA	SAUIC A. N., KROLL K. L., EVANS L. M., KIRSCHNER M. W.,
Qy	273	VKRWQKGOREFKRSRSRKLQG	295							RL	SEQUEL DEVELOPMENT 124:4739-4748(1997).
		[1]								DR	SAUIC A. N., KROLL K. L., EVANS L. M., KIRSCHNER M. W.,
Db	85	LFAPVCLDTF--IQPCVTPTEMACNDGYSEMRLPMLNMGHTNAEVYKPSAEMQNLLQGTCHPYARTFLCS	141							SQ	SEQUEL DEVELOPMENT 124:4739-4748(1997).
Qy	98	LFAPVCLDTF--IQPCVTPTEMACNDGYSEMRLPMLNMGHTNAEVYKPSAEMQNLLQGTCHPYARTFLCS	84							RA	SAUIC A. N., KROLL K. L., EVANS L. M., KIRSCHNER M. W.,
		[1]								DR	SEQUEL DEVELOPMENT 124:4739-4748(1997).
Db	142	KEYQY-SKKELPKPKSCGCLIEEFSHKTVLEAFCDNFAVYKVLAKKKS-GH-YEY	198							SQ	SEQUEL DEVELOPMENT 124:4739-4748(1997).
RESULT	10	PRELIMINARY;	PRT;	307	AA.					RA	SAUIC A. N., KROLL K. L., EVANS L. M., KIRSCHNER M. W.,
ID	042397;									DR	SEQUEL DEVELOPMENT 124:4739-4748(1997).
AC	042397;									SQ	SEQUEL DEVELOPMENT 124:4739-4748(1997).
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)									RA	SAUIC A. N., KROLL K. L., EVANS L. M., KIRSCHNER M. W.,
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)									DR	SEQUEL DEVELOPMENT 124:4739-4748(1997).

Qy 158 SDHLLPATEAAPK -VCEACKNNKND -DDNDIMETLCKNDFAALKVKBITYINRDTKIL 214  
 Db 199 ETEGPVEFIKQGULLPYDTRTMEQWLLINENCAQKLJRTTRTPVYVIAEGIHGKVKNR 258  
 Qy 215 ETKSKTIVKLNQYSER -DLKKSY -LWLDSQCTCEEMNDINAPYLYMGQKQGELVITS 272  
 Db 259 IETHWQKQADSQTLATRMRHHKC 281  
 Qy 273 VWRWQKQREFKRISRSRKLOC 295

RESULT 12  
 ID 016147 PRELIMINARY; PRT; 568 AA.  
 AC DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
 DT 01-JUN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
 DE 06-NOV-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 GN MOM-5.  
 OS CAENORHABDITIS ELEGANS.  
 OC EUKARYOTA; METAZOA; ACELOMATES; NEMATODA; SECERNENTIA; RHABDITIDA.  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RC STRAIN=BRISTOL;  
 RX MEDLINE; 97433081.  
 RA ROCHELEAU C. E., DOWNS W.D., LIN R., WITTMANN C., BEI Y., CHA Y. -H.,  
 RA ALI M., PRIESS J. R., MELO C.C.,  
 RL CELL 90:707-116 (1997).  
 DR EMBL; AF013953; G2463674;  
 SQ SEQUENCE 568 AA; 62892 MW; 8578BB4F CRC32;

Query Match Score 400; DB 568; Length 568;  
 Best Local Similarity 37.4%; Pred. No. 4.58e-68;  
 Matches 58; Conservative 33; Mismatches 54; Indels 10; Gaps 8;

Db 5 IILIFLFG -CLSDAQRLSSTSISMMNGFSTTR-KCEHI-T -IPMCKNLDYNOTVFPNLL 59  
 Qy 8 LILFLASHCCCLGSA -R -GLFLFGQDPSYSKRNSNCRKPIANQOLCHIEYQNMRLPNLL 64  
 Db 60 GHTTOSBAGPAIAQFNPLIKVCSERDLFLCIVYAPVC -TyleKPIOPCREUCLSAKNG 118  
 Qy 65 GHETMKVELEQAGAWIPLVMKQCHPDTKKEFLSLFAPYCLDDLETOPICHSLCQVQYKDR 124  
 Db 119 CEPSLMKKEFGFQWDPDQDCNKFVY-TDLCVGKNSSE 152  
 Qy 125 CAPVMSAFGEFPNPDMLECDRFP-ODNDIPLASSD 159

RESULT 13  
 ID 057328 PRELIMINARY; PRT; 592 AA.  
 AC DT 01-JUN-1998 (TREMBLREL. 06, CREATED)  
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)  
 DE 06-NOV-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
 DE 7-TRANSMEMBRANE FRIZZLED-1.  
 GN F2-1.  
 OS GALLUS GALLUS (CHICKEN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AVES; NEOGNATHAE.  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RC TISSUE=LIMB BUD;  
 RA KENGAKU M., TWOMBLY V., TABIN C.;  
 RL COLD SPRING HARB. SYMP. QUANT. BIOL. 0:0-0 (1997).  
 DR EMBL; AF031030; G26555274;  
 KW TRANSMEMBRANE.  
 SQ SEQUENCE 592 AA; 65490 MW; CD66ECB3 CRC32;

Query Match Score 397; DB 13; Length 592;  
 Best Local Similarity 37.7%; Pred. No. 2.49e-67;  
 Matches 49; Conservative 32; Mismatches 44; Indels 5; Gaps 5;

Db 67 HGYCQPI-S-IPCLTDIAYNOTIMPNLIGHTNQEDAGLEVHQFYPLVYQGCHSHLRFRLCLSYAPNC 124

Qy 37 RSNCKPANOLQCHGIXYQNMRLPNLIGHETMKEVLLQAGAVIPLVYQCHPDTKPKIC 96  
 Db 125 SMVAPVC-TYLEQALPPPSLCEBARQGCEALMNKGQFWPDTRCEKPVHAGELCVG 183  
 Qy 97 SLFAPVCLDDLDDETIQPHSCLCVQVDRCAPVMSAFGPFWPDMLECDRFP -QDN -DLCIP 154  
 Db 184 QNSASERGPT 193  
 Qy 155 LASSDHLLPA 164

RESULT 14  
 ID 061090 PRELIMINARY; PRT; 572 AA.  
 AC DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-JAN-1998 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DE 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
 DE FRIZZLED HOMOLOG 7 (TRANSMEMBRANE RECEPTOR).  
 GN F2D7 OR FRIZZLED 7.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RX MEDLINE; 96224032.  
 RA WANG Y., MACKE J.P., ABELLA B.S., ANDREASSON K., WORLEY P.,  
 RA GILBERT D.J., COPELAND N.G., JENKINS N. A., NATHANS J.;  
 RL J. BIOL. CHEM. 271:4468-4476 (1996).  
 DR EMBL; U43320; G1151258; -.  
 DR MGDB; MG1:108570; F2D7.  
 KW TRANSMEMBRANE.  
 SQ SEQUENCE 572 AA; 63816 MW; FA1D78D2 CRC32;

Query Match Score 396; DB 11; Length 572;  
 Best Local Similarity 40.7%; Pred. No. 4.38e-67;  
 Matches 48; Conservative 42; Mismatches 42; Indels 3; Gaps 3;

Db 51 PISIPCLCTDIAYNOTIPLLGLHQNEDAGLEVHQFYPLVYQOSPELRFCLCSYAPVC 110  
 Qy 44 PANIQOLCHGIEYQNMRLPNLIGHETMKEVLLQAGAWIPLVYQCHPDTKPKLSSLFAPVC 103  
 Db 111 -TVLDQATIPPCRSCLCERAQGCEALMNKGQFWPDTRCEKPVHAGELCVGQNTSD 167  
 Qy 104 LDDLDDETIQPHSCLCVQVDRCAPVMSAFGPFWPDMLECDRFP -QDN -DLCIPLASSD 159

RESULT 15  
 ID 000144 PRELIMINARY; PRT; 591 AA.  
 AC 000144  
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)  
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
 DE FRIZZLED HOMOLOG.  
 GN F2D3.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RX MEDLINE; 97227293.  
 RA WANG Y. K., HARRYMAN SAMOS C., PEOPLES R., PEREZ-JURADO L. A., NUSSE R.,  
 RA FRANKE U.;  
 RL HUM. MOL. GENET. 6:465-472 (1997).  
 DR EMBL; U82169; G1905598;  
 SQ SEQUENCE 591 AA; 64466 MW; 88C5EC1F CRC32;

Query Match Score 394; DB 4; Length 591;  
 Best Local Similarity 37.3%; Pred. No. 1.35e-66;  
 Matches 48; Conservative 32; Mismatches 47; Indels 1; Gaps 1;

Db 41 AVEIPMCRGIGYGNLTRMPNLLGHTSQGQAAELAEFAPLVQYQGCHSHLRFRLCLSYAPNC 100  
 Qy 105 LDDLDDETIQPHSCLCVQVDRCAPVMSAFGPFWPDMLECDRFP -QDN -DLCIPLASSD 159

Qy	44	PANLQLQHGEYQNMQLRPLNQLIGHETMKVEVLBDAGAWIPLVNRQCHD7KKFLCSLAPVC 103
Db	101	TDQVSTPIAPCRPMCFOARLRCAPIMEQFNFGWPSLDCARLPTTRNDPHALCMEAOPENAT 160
Qy	104	LDDLDIETIQPCHSVLCYQVKDRCAVPMASFGEFWPDMECDRFPOONDLCIPLASSDHLL 162
Db	161	AGPAAEHHK 168
Ov	163	PATFPEAK 170

search completed: Thu Oct 22 15:52:56 1998  
Job time : 87 secs.



Qy 24 PANLQLCHGIEYONMRLLPNLGHETMKVELEGAGAWIPLVMKOCHPDTKKFLCSLFAFVC 83  
 Db 111 -tvldegapprslcerarggealmnkkgfgyperlrcnfpvhgagcicygntsd 167  
 Qy 84 LDDDETIQPCHSCLCVQVRDRCAVMSAFGFPWMDMLECDRFP-QDN-DLCIPLASSD 139

**RESULT<sup>2</sup>**  
 ID W31274 standard; Protein: 685 AA.  
 AC W31274\_2; English.  
 DT 27-APR-1998 (first entry).  
 DE Mouse frizzled-8 protein Mfz8 (Wnt receptor).  
 KW Wnt receptor; mouse frizzled-8 protein; Mfz8 gene;  
 KW signal transduction; cancer; cell growth; cell proliferation.  
 OS Mus musculus.  
 PN W0973957-A1.  
 PD 23-OCT-1997.  
 PF 11-APR-1997; U06049.  
 PR 12-APR-1996; US-015307.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J,  
 PI Nusse R, Santos CH, Wangy;  
 DR N-PSDB; T89892.  
 PT Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation related disorders  
 Disclosure; Page 48-50; 61pp; English.  
 This Protein comprises the mouse transmembrane receptor, frizzled-8 (Mfz8), encoded by the Mfz8 gene (see T89892). It is an example of a Wnt receptor. Other novel frizzled family members have been identified in human, mouse and *Caenorhabditis elegans* (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.

Qy 25 PANLQLCHGIEYONMRLLPNLGHETMKVELEGAGAWIPLVMKOCHPDTKKFLCSLFAFVC 83  
 Db 111 -tvldegapprslcerarggealmnkkgfgyperlrcnfpvhgagcicygntsd 167  
 Qy 84 LDDDETIQPCHSCLCVQVRDRCAVMSAFGFPWMDMLECDRFP-QDN-DLCIPLASSD 139

**RESULT<sup>3</sup>**  
 ID W31271 standard; Protein: 585 AA.  
 AC W31271\_3; English.  
 DT 27-APR-1998 (first entry).  
 DE Human frizzled-5 protein Mfz5 (Wnt receptor).  
 KW Wnt receptor; human frizzled-5 protein; Mfz5 gene;  
 KW signal transduction; cancer; cell growth; cell proliferation.  
 OS Homo sapiens.  
 PN W0973957-A1.  
 PD 23-OCT-1997.  
 PR 11-APR-1997; U06049.  
 PR 12-APR-1996; US-015307.  
 PA (UYJO ) UNIV JOHNS HOPKINS.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J,  
 PI Nusse R, Santos CH, Wangy;  
 DR N-PSDB; T89892.  
 PT Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation related disorders  
 Disclosure; Page 37-39; 61pp; English.  
 This protein comprises the human transmembrane receptor, frizzled-5 (Hfz5), encoded by the Hfz5 gene (see T89892). It is an example of a Wnt receptor. Other novel frizzled family members have been identified in human, mouse and *Caenorhabditis elegans* (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.

Qy 26 PANLQLCHGIEYONMRLLPNLGHETMKVELEGAGAWIPLVMKOCHPDTKKFLCSLFAFVC 83  
 Db 111 -tvldegapprslcerarggealmnkkgfgyperlrcnfpvhgagcicygntsd 167  
 Qy 84 LDDDETIQPCHSCLCVQVRDRCAVMSAFGFPWMDMLECDRFP-QDN-DLCIPLASSD 139

**RESULT<sup>4</sup>**  
 ID W31270 standard; Protein: 537 AA.  
 AC W31270\_4; English.  
 DT 27-APR-1998 (first entry).  
 DE Mouse frizzled-4 protein Mfz4 (Wnt receptor).  
 KW Wnt receptor; mouse frizzled-4 protein; Mfz4 gene;  
 KW signal transduction; cancer; cell growth; cell proliferation.

Qy 27 PANLQLCHGIEYONMRLLPNLGHETMKVELEGAGAWIPLVMKOCHPDTKKFLCSLFAFVC 83  
 Db 40 VPIckgignytymqnpqfnhdgtdeaglevhqvfpw-pleiveiqspdkfflcsmytpicle 98  
 Qy 27 LQQLCHGIEYONMRLLPNLGHETMKVELEGAGAWIPLVMKOCHPDTKKFLCSLFAFVC 85

Qy 28 PANLQLCHGIEYONMRLLPNLGHETMKVELEGAGAWIPLVMKOCHPDTKKFLCSLFAFVC 85  
 Db 99 dykkpippccrscceratagcaplmrgyfawmpdrmrdrpdrqgnpd1lcmgnrtd-1t 157  
 Qy 86 DLDDETIQPCHSCLCVQVRDRCAVMSAFGFPWMDMLECDRFP-QDN-D-LCIPPLASSD 142

Qy 158 taapsppr 165  
 Qy 143 PATEEAKP 150

Qy 29 PANLQLCHGIEYONMRLLPNLGHETMKVELEGAGAWIPLVMKOCHPDTKKFLCSLFAFVC 83  
 Db 111 -tvldegapprslcerarggealmnkkgfgyperlrcnfpvhgagcicygntsd 167  
 Qy 84 LDDDETIQPCHSCLCVQVRDRCAVMSAFGFPWMDMLECDRFP-QDN-D-LCIPPLASSD 139

**RESULT<sup>5</sup>**  
 ID W31271 standard; Protein: 585 AA.  
 AC W31271\_5; English.  
 DT 27-APR-1998 (first entry).  
 DE Human frizzled-5 protein Mfz5 (Wnt receptor).  
 KW Wnt receptor; human frizzled-5 protein; Mfz5 gene;  
 KW signal transduction; cancer; cell growth; cell proliferation.  
 OS Homo sapiens.  
 PN W0973957-A1.  
 PD 23-OCT-1997.  
 PR 11-APR-1997; U06049.  
 PR 12-APR-1996; US-015307.  
 PA (UYJO ) UNIV JOHNS HOPKINS.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J,  
 PI Nusse R, Santos CH, Wangy;  
 DR N-PSDB; T89892.  
 PT Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation related disorders  
 Disclosure; Page 34-35; 61pp; English.  
 This protein comprises the mouse transmembrane receptor, frizzled-4 (Mfz4), encoded by the Mfz4 gene (see T89892). It is an example of a Wnt receptor. Other novel frizzled family members have been identified in human, mouse and *Caenorhabditis elegans* (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for



Wnt receptor; mouse frizzled-3 protein; Mfz3 gene; signal transduction; cancer; cell growth; cell proliferation. MUS musculus. WO9739357-A1. 23-OCT-1997. 006049. 11-APR-1997. 006049. 12-APR-1996. US-015307. (UYJO) UNIV JOHNS HOPKINS. (STRD) UNIV LEELAND STANFORD JUNIOR. Andrew D., Blanot P., Brink M., Hsieh J., Nathans J., Nusse R., Samos CH., Wang J.; WPI: 97-52631/48. N-PSDB/T8986.

Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation disorders. Disclosure; page 27-29; 61pp; English. This protein comprises the mouse frizzled-3 protein encoded by the Mfz3 gene (see T8986), and is a Wnt receptor. Other novel frizzled family members have been identified in human, mouse *Ceenorhabditis elegans* (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions. 666 AA: sequence.

8  
 RESULT  
 W31272 standard; Protein: 709 AA.  
 W31272;  
 27-APR-1998 (first entry)  
 Mouse frizzled-6 protein Mfz6 (Wnt receptor).  
 Wnt receptor; mouse frizzled-6 protein; Mfz6 gene;  
 signal transduction; cancer; cell growth; cell proliferation.  
 Mus musculus.  
 WO0739157-A1.  
 23-OCT-1997.  
 11-APR-1997 006049.  
 12-APR-1996 US-015307.  
 (UYJO ) UNIV JOHNS HOPKINS.  
 (STRD ) UNIV LEILAND STANFORD JUNIOR.  
 Andrew D., Blanot P., Brink M., Hsieh J., Nathans J.,  
 Nusse R., Santos CH., Wangy;  
 WPI: 97-526531/48.  
 N-PSDB: T89990.  
 Identification of Wnt receptor binding modulators - useful for  
 treatment of cancer and growth, development or proliferation  
 disorders  
 disclosure: Page 41-42; 61pp; English.  
 This protein comprises the mouse putative transmembrane recep-  
 tor frizzled-6 (Mfz6), encoded by the Mfz6 gene (see T89980). It  
 is an example of a Wnt receptor. Other novel frizzled family mem-  
 bers have been described.

have been identified in human, mouse and *Caenorhabditis elegans* (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.

Query Match	13.7%	Score 284;	DB 27;	Length 709;
Best Local Similarity	33.68;	Pred. No. 3.89e-17;		
Matches	26;	Mismatches	49;	Indels 6;
Matches	41;	Conservative		Gaps 6;
Db	24	cepitvp-r-cmkntky-nntffpnlgmghdqqitavenghflhanlecsnpiemflcqg 80		
Qy	20	CKPITANLQCHLGEYQNRRN-PNLIGHETMKVEYEQAGAWIPLYMKQCHPDTKFLCSL 78		
Db	81	fipteqeinh-vvlpccrk1cekiyvsdckklmdtfgirwpeelecnrphcdt-vpvtsh 138		
Qy	79	FAPVYCLDDLETIQPHS1CQVQKDRCAPYMSAEGFPWDMLECDRFPQNDLCPPLASS 138		
Db	139	ph 140		
Qy	139	DH 140		

Matches	30	Conservative	28	Mismatches	46	Indels	7	Gaps	6
RESULT	10								
ID	R71186	standard:	Protein:	605	AA.				
AC	R71186;								
DT	24-DEC-1995	(First entry)							
Check	p78.								
KW	Neural axon out-growth modulator; epidermal growth factor; EGF;								
KW	neuin-1; p78; neurodegenerative disease; transgenic animal;								
KW	gene therapy.								
OS	Gallus sp.								
PFH	peptide	1..25	Location/Qualifiers						
PFH	peptide		/label= Sig-peptide						
FFT	miss_difference	29							
FFT	miss_difference		/note= "unspecified amino acid"						
FFT	miss_difference	38							
FFT	miss_difference		/note= "unspecified amino acid"						
FFT	miss_difference	50							
FFT	miss_difference		/note= "unspecified amino acid"						
domain	domain	26..284	/label= Domain-VI						
FFT	domain		/note= "Domain VI is probably involved in protein-						
FFT	domain		protein complex formation."						
FFT	domain	285..453	/label= Domain-V						
FFT	domain		/note= "domain V includes EGF-1-like repeats"						
FFT	region	454..605	/note= "C-terminal region"						
FFT	region								
PN	W09513367-A1.								
PN	18 MAY 1995.								
PN	08 NOV-1994.								
PPR	12 NOV-1993;		012913.						
PPR	US-152019.								
PPA	(RESC )	UNIV CALIFORNIA.							
PPA	(UCCO )	UNIV COLUMBIA, NEW YORK.							
PS	Dodd J	Jesseell T, Kennedy T,	Placzek M,	Serafini T;					
PS	Tessier-Lavigne M;								
PS	WPI: 95-194086/25.								
DR	N-PSDB; Q92366.								
PPT	Neural axon out-growth modulators derived from EGF-like repeats of								
PPT	neuin 1 or neuin 2 - comprise peptide(s) capable of selectively								
PPT	increasing spinal axon out-growth or directing axon orientation								
PS	Claim 1; Page 44-46; 58pp; English.								
PS	An E10 chick brain cDNA library was screened with probes based on								
PS	neuin-1 (p78) or neuin-2 (p75) sequences to isolate chick p78								
PS	and p75 partial cDNA clones. Full-length clones (given in								
PS	Q92366-67, respectively) were subsequently obt'd. by 3'-RACE, cDNA								
PS	is expressed e.g. in COS or insect cells for recombinant p78 and								
PS	p75 prodr., used to breed transgenic animals, or for gene therapy.								
PSQ	Sequence 605 AA:								
Query	Match	6.0%	Score 124;	DB 14;	Lenght 605;				
Matches	Best Local Similarity	26.1%	Pred. No. 3	93e-02;					
Matches	Conservative	31;	Mismatches	41;	Indels	13;	Gaps	11	
Qy	133	IPASSDHLLPATEEAPKVCEA-CKNRNDDDIMETICKNDFAKVKY-KEITYINRDT	191						
Ddb	455	1paappptbassteepad-cdsyckasgk1kinmkkyckkdkyavqhilkaeknadv-w	512						
Qy	133	IPASSDHLLPATEEAPKVCEA-CKNRNDDDIMETICKNDFAKVKY-KEITYINRDT	190						
Ddb	513	kftvnlis--vyk-99-snrs-lrrgdotlwahdiackcpkmkk-yl11gsts	565						
Qy	191	KIETKSKTIYKLNGVSERDLKSVLWLK-DSLQCTEEMNDINAPPVLMG	246						

PN	W09513367-A1.	Best Local Similarity	30.5%	Pred. No.	3.78e+00;
PD	18-MAY-1995.	Matches	25;	Conservative	15;
PF	08-NOV-1994; U12913.	Mismatches	36;	Indels	6;
PR	12-NOV-1993; US-152019.	Gaps	5;		
PA	(REGC ) UNIV CALIFORNIA.				
(UYCO ) UNIV COLUMBIA NEW YORK.					
Dodd J., Jessell T., Kennedy T., Placzek M., Serafini T;					
PT					
PI					
Tessier-Lavigne M.					
DR	WPI: 95-194086/25.				
DR	N-PSDB: 092368.				
PT	Neural axon out-growth modulators derived from EGF-like repeats of				
PT	neuin 1 or neuin 2 - comprise peptide(s) capable of selectively				
PT	increasing spinal axon out-growth or directing axon orientation				
PS	Claim 1; Page 51; 58pp; English.				
CC	Chick P75 and P78 sequences (given in R74186-87, respectively)				
CC	were used to identify conserved amino acid regions, which were				
CC	then used to design degenerate primers for the amplification				
CC	of a fragment of the mouse P78 cDNA (092368). This cDNA can				
CC	be expressed in host cells for recombinant P78 prodn, or used				
CC	to breed transgenic animals, or for gene therapy.				
SQ	Sequence 529 AA;				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Db	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
	Best Local Similarity	23.5%	Length	529;	
	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				
Db	445 vykqgtsrirrgdqs-1wirsdiackopkplkk-yllg 484				
Qy	201 IYKLNGYSERDLKKSVLWLD-SLQCTCEEMNDINAPLYMG 241				
Query Match	5.1%	Score	105;	DB	14;
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	Matches	24;			
	Conservative	25;			
	Pred. No.	1.50e+00;			
	Mismatches	45;			
	Indels	8;			
	Gaps	7;			
Db	388 sxeveexcdcsyckaskgkglmmkkycrkdyavghihlkdkaggw-wkftvnlis-- 444				
Qy	143 PATEEAPRKVCEA-CKNNNDDDNDIMETLICKNDALKIKV-KETTYINRDTKFILETSKT 200				

KW Enzyme; cyclosporin; synthetase-like activity; Tolypocladium niveum;  
 KW T. inflatum GAMS; biosynthesis; vector; cyclosporin synthetase.  
 OS Tolypocladium niveum.  
 PN EP-578616-A.  
 PD 12-JAN-1994.  
 PF 05-JUL-1992; 810474.  
 PR 09-JUL-1992; AT-001403.  
 PR 08-MAR-1993; AT-000437.  
 PR 29-AFR-1993; CH-001310.  
 PR 04-MAY-1993; CH-001375.  
 PA (SANO ) SANDOZ LTD.  
 PA (SANO ) SANDOZ PATENT GMBH.  
 PA (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.  
 PI Leitner E, Schneider E, Schoergendorfer K, Weber G;  
 WPI 94-010432/02.  
 DR N-PSDB: Q54386.  
 PT Isolated DNA sequence - which codes for enzyme having cyclosporin  
 PT synthetase like activity  
 PS Claim 1: Page 41-84; 93pp; English.  
 CC This sequence represents an enzyme which has cyclosporin synthetase-  
 like activity. This sequence was isolated from Tolypocladium niveum  
 (formerly known as T. inflatum GAMS). This enzyme catalyses the  
 peptide biosynthesis of cyclosporins and structurally related  
 molecules. This sequence may be used for the production of  
 cyclosporin by transforming a vector containing this sequence in  
 to a recombinant host. This allows effective production of anti-  
 biotic cyclosporin or its derivatives.  
 SQ Sequence 15281 AA;

Query Match Score 97; DB 9; Length 15211;  
 Best Local Similarity 4.7%; Pred. No 6.52e+00; Gaps 8;  
 Matches 24; Conservative 23; Mismatches 35; Indels 8;  
 Db 3819 lrgtkisdhiaanipnsktiverticesydlgg-dakdsndrvawlsaa-rsnavkva 3876  
 Qy 176 LK-IVYKE-ITYIN-RDTKIL-E-TKSNTYKLNGYSERDLKKSVLWLKDSDQCTCEEMN 231  
 Db 3877 s1satd1vdiaqeqfrveiscarqwsqng 3906  
 Qy 232 DINAPYLV-MGQKQGELVITSVKRW-QKG 259

Search completed: Thu Oct 22 16:01:16 1998  
 Job time : 70 secs.